

STIC-Biotech/ChemLib

105381

From: Bunner, Bridget  
Sent: Monday, October 06, 2003 9:42 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like to request a sequence search for case 10/070,240:

1. the amino acid sequence of SEQ ID NO: 1

Thanks!

Bridget Bunner

Art Unit 1647  
CM1-10D12  
(703) 305-7148  
mailbox 10B19

OCT 6 2003  
STIC

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 10/7/03  
Date Completed: 10/8/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 02  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 09:52:17 ; Search time 67 Seconds  
(without alignments)  
928.025 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTWGPMDDNATNTSFL.....LDLKTIGMPATEEVDICRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description      |
|------------|--------|-------------|--------|-------|------------------|
| 1          | 2055   | 100.0       | 393    | 9     | US-09-750-373-26 |
| 2          | 2055   | 100.0       | 393    | 12    | US-10-088-726-4  |
| 3          | 2055   | 100.0       | 393    | 15    | US-10-067-649-2  |
| 4          | 2035   | 99.0        | 389    | 9     | US-09-750-373-27 |
| 5          | 2035   | 99.0        | 389    | 10    | US-09-925-922-2  |
| 6          | 2035   | 99.0        | 389    | 15    | US-09-925-922-4  |
| 7          | 2030   | 98.8        | 389    | 12    | US-10-445-680-35 |
| 8          | 1924   | 93.6        | 382    | 15    | US-10-132-812-6  |
| 9          | 1766   | 85.9        | 384    | 12    | US-10-321-807-2  |
| 10         | 1766   | 85.9        | 384    | 15    | US-10-132-812-4  |
| 11         | 1764   | 85.8        | 393    | 15    | US-10-067-649-4  |
| 12         | 1762   | 85.7        | 384    | 9     | US-09-764-556-2  |
| 13         | 1762   | 85.7        | 384    | 15    | US-10-132-812-2  |
| 14         | 1755.5 | 85.4        | 385    | 15    | US-10-220-289-5  |
| 15         | 1703   | 82.9        | 355    | 15    | US-10-067-649-3  |

|    |       |      |     |    |                     |                    |
|----|-------|------|-----|----|---------------------|--------------------|
| 16 | 1109  | 54.0 | 231 | 15 | US-10-220-289-4     | Sequence 4, Appli  |
| 17 | 1042  | 50.7 | 207 | 11 | US-09-782-974C-34   | Sequence 34, Appl  |
| 18 | 839   | 40.8 | 254 | 12 | US-10-017-161-1548  | Sequence 1548, Ap  |
| 19 | 799   | 38.9 | 217 | 9  | US-09-750-373-19    | Sequence 19, Appl  |
| 20 | 657   | 32.0 | 154 | 15 | US-10-220-289-2     | Sequence 2, Appli  |
| 21 | 589   | 28.7 | 123 | 9  | US-09-864-761-36840 | Sequence 36840, A  |
| 22 | 589   | 28.7 | 123 | 9  | US-09-864-761-48506 | Sequence 48506, A  |
| 23 | 431   | 21.0 | 86  | 10 | US-09-925-922-4     | Sequence 4, Appli  |
| 24 | 416.5 | 20.3 | 385 | 15 | US-10-067-649-6     | Sequence 6, Appli  |
| 25 | 407   | 19.8 | 464 | 12 | US-10-283-423-14    | Sequence 14, Appl  |
| 26 | 407   | 19.8 | 464 | 12 | US-10-213-821-14    | Sequence 14, Appl  |
| 27 | 407   | 19.8 | 518 | 12 | US-10-383-423-16    | Sequence 16, Appl  |
| 28 | 407   | 19.8 | 518 | 12 | US-10-213-821-16    | Sequence 16, Appl  |
| 29 | 401.5 | 19.5 | 381 | 12 | US-10-188-619-4     | Sequence 4, Appli  |
| 30 | 401.5 | 19.5 | 381 | 15 | US-10-067-649-5     | Sequence 5, Appli  |
| 31 | 395.5 | 19.2 | 381 | 12 | US-10-188-619-6     | Sequence 6, Appli  |
| 32 | 390.5 | 19.0 | 385 | 11 | US-09-992-331-18    | Sequence 18, Appl  |
| 33 | 390.5 | 19.0 | 385 | 16 | US-10-262-313-18    | Sequence 18, Appl  |
| 34 | 387.5 | 18.9 | 381 | 10 | US-09-962-646-16    | Sequence 16, Appl  |
| 35 | 387.5 | 18.9 | 381 | 10 | US-09-992-973-5     | Sequence 5, Appli  |
| 36 | 387.5 | 18.9 | 381 | 10 | US-09-992-973-20    | Sequence 20, Appli |
| 37 | 387.5 | 18.9 | 381 | 12 | US-10-188-619-2     | Sequence 2, Appli  |
| 38 | 387.5 | 18.9 | 381 | 15 | US-10-225-567A-201  | Sequence 201, App  |
| 39 | 382   | 18.6 | 522 | 12 | US-10-283-423-12    | Sequence 12, Appl  |
| 40 | 382   | 18.6 | 522 | 12 | US-10-213-821-12    | Sequence 12, Appl  |
| 41 | 380.5 | 18.5 | 519 | 12 | US-10-283-423-10    | Sequence 10, Appl  |
| 42 | 380.5 | 18.5 | 519 | 12 | US-10-213-821-10    | Sequence 10, Appl  |
| 43 | 370   | 18.0 | 370 | 12 | US-10-278-087A-26   | Sequence 26, Appl  |
| 44 | 370   | 18.0 | 370 | 14 | US-10-044-592-12    | Sequence 12, Appl  |
| 45 | 370   | 18.0 | 370 | 14 | US-10-044-592-74    | Sequence 74, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-750-373-26  
; Sequence 26, Application US/09750373  
; Patent No. US20020062013A1  
; GENERAL INFORMATION:  
; APPLICANT: Lind Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Hiebsch, Ronald  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Lindberg, Eleni  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Vogeli, Gabriel  
; TITLE OF INVENTION: No. US20020062013A1el G Protein Coupled Receptors  
; FILE REFERENCE: PHRM-0300  
; CURRENT APPLICATION NUMBER: US/09/750,373  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/188,880  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/219,492  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: 60/173,339  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/224,321  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/200,534  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/239,062  
; PRIOR FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-750-373-26

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Query Match      100.0%; Score 2055; DB 9; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.7e-188;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTTMGFMDDNATNTSTFSLVLPNPHGAHATSPFPNFSDYDMPDDEDEDVNSRTFFA 60
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DB 1 MTTMGFMDDNATNTSTFSLVLPNPHGAHATSPFPNFSDYDMPDDEDEDVNSRTFFA 60
   |||

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||
DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||

QY 121 DYYVYRQLSWEHGHVLTCSVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMKCOTAT 180
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DB 121 DYYVYRQLSWEHGHVLTCSVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMKCOTAT 180
   |||

QY 181 GLIALVMTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
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DB 181 GLIALVMTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
   |||

QY 241 FVGPPVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLLMCLITATVYLCWAPF 300
   |||
DB 241 FVGPPVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLLMCLITATVYLCWAPF 300
   |||

QY 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFTVYKNDTVKYFKKIMLLH 360
   |||
DB 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFTVYKNDTVKYFKKIMLLH 360
   |||

QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
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DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
   |||

RESULT 2
US-10-088-726-4
; Sequence 4, Application US/10088726
; Publication No. US2003015758A1
; GENERAL INFORMATION:
; APPLICANT: Matsumoto et al.
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AND
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088, 726
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/JP00/09408
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 1999-375152
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: JP 2000-101339
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-088-726-4

Query Match      100.0%; Score 2055; DB 12; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.7e-188;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTTMGFMDDNATNTSTFSLVLPNPHGAHATSPFPNFSDYDMPDDEDEDVNSRTFFA 60
   |||
DB 1 MTTMGFMDDNATNTSTFSLVLPNPHGAHATSPFPNFSDYDMPDDEDEDVNSRTFFA 60
   |||

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||
DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||

QY 121 DYYVYRQLSWEHGHVLTCSVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMKCOTAT 180
   |||
DB 121 DYYVYRQLSWEHGHVLTCSVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMKCOTAT 180
   |||
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QY 181 GLIALVMTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
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DB 181 GLIALVMTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
   |||

QY 241 FVGPPVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLLMCLITATVYLCWAPF 300
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DB 241 FVGPPVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLLMCLITATVYLCWAPF 300
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QY 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFTVYKNDTVKYFKKIMLLH 360
   |||
DB 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFTVYKNDTVKYFKKIMLLH 360
   |||

QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
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DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
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RESULT 3
US-10-067-649-2
; Sequence 2, Application US/10067649
; Publication No. US20030100057A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM14, RELATED :
; FILE REFERENCE: D0118 NP
; CURRENT APPLICATION NUMBER: US/10/067,649
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266,525
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/329,897
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-649-2

Query Match      100.0%; Score 2055; DB 15; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.7e-188;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTTMGFMDDNATNTSTFSLVLPNPHGAHATSPFPNFSDYDMPDDEDEDVNSRTFFA 60
   |||
DB 1 MTTMGFMDDNATNTSTFSLVLPNPHGAHATSPFPNFSDYDMPDDEDEDVNSRTFFA 60
   |||

QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||
DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||

QY 121 DYYVYRQLSWEHGHVLTCSVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMKCOTAT 180
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DB 121 DYYVYRQLSWEHGHVLTCSVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMKCOTAT 180
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QY 181 GLIALVMTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
   |||
DB 181 GLIALVMTVSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDQQLYKSYFLFIFGIE 240
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QY 241 FVGPPVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLLMCLITATVYLCWAPF 300
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DB 241 FVGPPVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLLMCLITATVYLCWAPF 300
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QY 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFTVYKNDTVKYFKKIMLLH 360
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DB 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFTVYKNDTVKYFKKIMLLH 360
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QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
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DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393
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## RESULT 4

US-09-750-373-27  
; Sequence 27, Application US/09750373  
; Patent No. US20020062013A1  
; GENERAL INFORMATION:  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Hiesch, Ronald  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Lindberg, Eleni  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Vogeli, Gabriel  
; TITLE OF INVENTION: No US20020062013A1 G Protein Coupled Receptors  
; FILE REFERENCE: PHRM-0300  
; CURRENT APPLICATION NUMBER: US/09/750,373  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-750-373-27

Query Match 99.0%; Score 2035; DB 9; Length 389;

Best Local Similarity 100.0%; Pred. No. 1.4e-186;

Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| DB | 1   | MGFMDDNATNTSTFSLVLPNGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV  | 60  |
| QY | 65  | IGMALVGMVLCGIGNFIFTAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV   | 124 |
| DB | 61  | IGMALVGMVLCGIGNFIFTAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV   | 120 |
| QY | 125 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA | 184 |
| DB | 121 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA | 180 |
| QY | 185 | LWTVSILIAIPSAFYTTETVLVIVKSOEKFQCGIWPVQDQLYKSYFLFIFGIEFVGP   | 244 |
| DB | 181 | LWTVSILIAIPSAFYTTETVLVIVKSOEKFQCGIWPVQDQLYKSYFLFIFGIEFVGP   | 240 |
| QY | 245 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAYVLCWAPFYGT | 304 |
| DB | 241 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAYVLCWAPFYGT | 300 |
| QY | 305 | IVRDFPFTVVKRKHLYTAFYIVECIAMNSMINTLCFTVTKNDTVKFKIMLLHWKAS    | 364 |
| DB | 301 | IVRDFPFTVVKRKHLYTAFYIVECIAMNSMINTLCFTVTKNDTVKFKIMLLHWKAS    | 360 |
| QY | 365 | YNGKSSADLDLKTIGMPATEEVDICRLK                                | 393 |
| DB | 361 | YNGKSSADLDLKTIGMPATEEVDICRLK                                | 389 |

## RESULT 5

## US-09-925-922-2

; Sequence 2, Application US/09925922  
; Patent No. US20020165380A1  
; GENERAL INFORMATION:  
; APPLICANT: Bard, Jonathan A.  
; TITLE OF INVENTION: DNA Encoding A Mammalian Receptor (fb4la) And Uses  
; FILE REFERENCE: 55182.app  
; CURRENT APPLICATION NUMBER: US/09/925,922  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 2  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-922-2

Query Match 99.0%; Score 2035; DB 10; Length 389;

Best Local Similarity 100.0%; Pred. No. 1.4e-186;

Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 5   | MGFMDDNATNTSTFSLVLPNGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV  | 64  |
| DB | 1   | MGFMDDNATNTSTFSLVLPNGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV  | 60  |
| QY | 65  | IGMALVGMVLCGIGNFIFTAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV   | 124 |
| DB | 61  | IGMALVGMVLCGIGNFIFTAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV   | 120 |
| QY | 125 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA | 184 |
| DB | 121 | VRQLSWEHGHVLTCSVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA | 180 |
| QY | 185 | LWTVSILIAIPSAFYTTETVLVIVKSOEKFQCGIWPVQDQLYKSYFLFIFGIEFVGP   | 244 |
| DB | 181 | LWTVSILIAIPSAFYTTETVLVIVKSOEKFQCGIWPVQDQLYKSYFLFIFGIEFVGP   | 240 |
| QY | 245 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAYVLCWAPFYGT | 304 |
| DB | 241 | VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRRTVLVLMCILTAYVLCWAPFYGT | 300 |
| QY | 305 | IVRDFPFTVVKRKHLYTAFYIVECIAMNSMINTLCFTVTKNDTVKFKIMLLHWKAS    | 364 |
| DB | 301 | IVRDFPFTVVKRKHLYTAFYIVECIAMNSMINTLCFTVTKNDTVKFKIMLLHWKAS    | 360 |
| QY | 365 | YNGKSSADLDLKTIGMPATEEVDICRLK                                | 393 |
| DB | 361 | YNGKSSADLDLKTIGMPATEEVDICRLK                                | 389 |

## RESULT 6

US-10-225-567A-678  
; Sequence 678, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 678  
; LENGTH: 389  
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-10-225-567A-678

Query Match      99.0%; Score 2035; DB 15; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.4e-186;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV 64
   |||
Db 1 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV 60
   |||

QY 65 IGMALVGMVLCVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 124
   |||
Db 61 IGMALVGMVLCVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 120
   |||

QY 125 VROLSEHGVLCTSVNLTSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 184
   |||
Db 121 VROLSEHGVLCTSVNLTSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 180
   |||

QY 185 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 244
   |||
Db 181 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 240
   |||

QY 245 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFT 304
   |||
Db 241 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFT 300
   |||

QY 305 IVRDFPPTVFKKHYLTAFYIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 364
   |||
Db 301 IVRDFPPTVFKKHYLTAFYIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 360
   |||

QY 365 YNGKSSADLDLKTIGMPATEEVDICRLK 393
   |||
Db 361 YNGKSSADLDLKTIGMPATEEVDICRLK 389
   |||

RESULT 7
US-10-345-680-35
; Sequence 35, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Venkateswari, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RNN.OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 389

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-345-680-35

Query Match      98.8%; Score 2030; DB 12; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.2e-186;
Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV 64
   |||
Db 1 MGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFAAKIV 60
   |||

QY 65 IGMALVGMVLCVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 124
   |||
Db 61 IGMALVGMVLCVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 120
   |||

QY 125 VROLSEHGVLCTSVNLTSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 184
   |||
Db 121 VROLSEHGVLCTSVNLTSLVSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIA 180
   |||

QY 185 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 244
   |||
Db 181 LWMTVSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 240
   |||

QY 245 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFT 304
   |||
Db 241 VVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFT 300
   |||

QY 305 IVRDFPPTVFKKHYLTAFYIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 364
   |||
Db 301 IVRDFPPTVFKKHYLTAFYIVKSEKIFCGQIWPVDQOLYKSYFIFIGIEFVGP 360
   |||

QY 365 YNGKSSADLDLKTIGMPATEEVDICRLK 393
   |||
Db 361 YNGKSSADLDLKTIGMPATEEVDICRLK 389
   |||

RESULT 8
US-10-132-812-6
; Sequence 6, Application US/10132812
; Publication No. US20030059856A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Sarau, Henry M.
; APPLICANT: Slemmon, J. Randall
; APPLICANT: McNulty, Dean E.
; APPLICANT: Vawter, Lisa
; APPLICANT: Foley, James J.
; TITLE OF INVENTION: Methods Of Screening For Agonists And
; TITLE OF INVENTION: Agonists Of The Interaction Between The AXOR8 And AXOR52
; TITLE OF INVENTION: Receptors And Ligands Thereof
; FILE REFERENCE: P51256
; CURRENT APPLICATION NUMBER: US/10/132,812
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,234
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-812-6

Query Match      93.6%; Score 1924; DB 15; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.8e-176;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTWGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFA 60
   |||
Db 1 MMTWGFMDNATNTSTFSLVNLPHGAHATSPFPNFYSYSDYDMPDDEDEDVNSRTFFA 60
   |||

QY 61 AKIVIGMALVGMVLCVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
   |||
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Db 61 AKIVGMAVGLMVCIGINFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
Qy 121 DYVVQLSWEHGHVLTSTVNLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180
Db 121 DYVVQLSWEHGHVLTSTVNLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180
Qy 181 GLIALVWTVSILIAISAYFTTETVLVIVKSOEKIFCGIWPVDOOLYKSYFLFIFGIE 240
Db 181 GLIALVWTVSILIAISAYFTTETVLVIVKSOEKIFCGIWPVDOOLYKSYFLFIFGIE 240
Qy 241 FVGPVVTMTLCYARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPF 300
Db 241 FVGPVVTMTLCYARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPF 300
Qy 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
Db 301 YGFTIVRDFPPTVFKKHYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
Qy 361 WKASYNG 367
Db 361 WKASYNG 367

RESULT 9
US-10-321-807-2
; Sequence 2, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Ruopong
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-2

Query Match 85.9%; Score 1766; DB 12; Length 384;
Best Local Similarity 87.4%; Pred. No. 7.8e-161;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 12 ATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVNSRTFFAAKIVIGMALVG 71
Db 3 AQNGNTSPTPNFPNPPQDHASSLSFNFSYDGLDLPDDEDEDMTKRTFFAAKIVIGIALG 62

Qy 121 ATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVNSRTFFAAKIVIGMALVG 71
Db 3 AQNGNTSPTPNFPNPPQDHASSLSFNFSYDGLDLPDDEDEDMTKRTFFAAKIVIGIALG 62

Qy 181 ATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVNSRTFFAAKIVIGMALVG 71
Db 3 AQNGNTSPTPNFPNPPQDHASSLSFNFSYDGLDLPDDEDEDMTKRTFFAAKIVIGIALG 62

Qy 361 WKASYNG 367
Db 361 WKASYNG 367
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Qy 72 IMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSWE 131
Db 63 IMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSWE 122
Qy 132 HGHVLTSTVNLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOATATGLIALVWTVSI 191
Db 123 HGHVLTSTVNLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOATATGLIALVWTVSI 182
Qy 192 LIAIPSAFTTETVLVIVKSOEKIFCGIWPVDOOLYKSYFLFIFGIEFVGPVVTMTLC 251
Db 183 LIAIPSAFTTETVLVIVKSOEKIFCGIWPVDOOLYKSYFLFIFGIEFVGPVVTMTLC 242
Qy 252 YARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFTIVRDFP 311
Db 243 YARISRELWFAVPGFQEQIRKRLCRKRTVLVLMCILTAIVLCWAPFYGFTIVRDFP 302
Qy 312 TVFVKEKHLYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLHWKASYNGKSS 371
Db 303 TVFVKEKHLYLTAFYIIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLHWKASYNGKSS 362
Qy 372 ADLKLKTIGMPATEEVDICRLK 393
Db 363 ADLKLKTIGMPATEEVDICRLK 384

RESULT 10
US-10-132-812-4
; Sequence 4, Application US/10132812
; Publication No. US20030059856A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Sarau, Henry M.
; APPLICANT: Slemon, J. Randall
; APPLICANT: McNulty, Dean E.
; APPLICANT: Vawter, Lisa
; APPLICANT: Foley, James J.
; TITLE OF INVENTION: Methods Of Screening For Agonists And
; TITLE OF INVENTION: Agonists Of The Interaction Between The AXOR8 And AXOR52
; TITLE OF INVENTION: Receptors And Ligands Thereof
; FILE REFERENCE: P51256
; CURRENT APPLICATION NUMBER: US/10/132,812
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,234
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-812-4

Query Match 85.9%; Score 1766; DB 15; Length 384;
Best Local Similarity 87.4%; Pred. No. 7.8e-161;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 12 ATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVNSRTFFAAKIVIGMALVG 71
Db 3 AQNGNTSPTPNFPNPPQDHASSLSFNFSYDGLDLPDDEDEDMTKRTFFAAKIVIGIALG 62

Qy 72 IMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSWE 131
Db 63 IMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSWE 122
Qy 132 HGHVLTSTVNLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOATATGLIALVWTVSI 191
Db 123 HGHVLTSTVNLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCOATATGLIALVWTVSI 182
Qy 192 LIAIPSAFTTETVLVIVKSOEKIFCGIWPVDOOLYKSYFLFIFGIEFVGPVVTMTLC 251
Db 183 LIAIPSAFTTETVLVIVKSOEKIFCGIWPVDOOLYKSYFLFIFGIEFVGPVVTMTLC 242
```

QY 252 YARISRELWFKAVPGFQTEQIRKRLCRKRTVILVLMCILTAIVLVCWAPFYGFTIVRDFEP 311  
DB 243 YARISRELWFKAVPGFQTEQIRKRLCRKRTVILVLMCILTAIVLVCWAPFYGFTIVRDFEP 302  
QY 312 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVYKFKIMLHWRKASVNGKSS 371  
DB 303 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVYKFKIMLHWRKASVNGKSS 362  
QY 372 ADDLKTGMPATEEVDICRLK 393  
DB 363 AELDLRTNGVPTATEEVDICRLK 384

## RESULT 11

US-10-067-649-4  
; Sequence 4, Application US/10067649  
; Publication No. US20030100057A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HDMN G-PROTEIN COUPLED RECEPTOR, HGPBMY14, RELATED TO  
; FILE REFERENCE: D0118 NP  
; CURRENT APPLICATION NUMBER: US/10/067,649  
; PRIOR FILING DATE: 2002-02-05  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-067-649-4

Query Match 85.8%; Score 1764; DB 15; Length 393;  
Best Local Similarity 84.0%; Pred. No. 1.2e-160;  
Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTGMFMDNATNTSTFSLVNLPHCAHATSPFNFSYSDYDMPDDEEDVTNSRTFFA 60  
DB 1 METTVGALGENTDTTDFESALDGHGATQSLPTFFESYDGYDMPDDEEDVTNSRTFFA 60  
QY 61 AKIVIGMALVGLVCGIGNFPIALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
DB 61 AKIVIGMALVGLVCGIGNFPIALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
QY 121 DYVYVRLSWHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180  
DB 121 DYVYVRLSWHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAA 180  
QY 181 GLIALVMTVSIILAIASVFTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFPIGIE 240  
DB 181 GLIFLVMSVSIILAIASVFTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFVFLV 240  
QY 241 FVGPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVILVLMCILTAIVLVCWAP 300  
DB 241 FVGPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVILVLMCILTAIVLVCWAP 300  
QY 301 YGFTIVRDFPPTVFKKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVYKFKIMLH 360  
DB 301 YGFTIVRDFPPTVFKKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVYKFKIMLH 360  
QY 361 WKASVNGKSSADLDTGMPATEEVDICRLK 393  
DB 361 WRASPSGSKASADLDTGMPATEEVDICRLK 393

## RESULT 12

US-09-764-556-2  
; Sequence 2, Application US/09764556  
; Patent No. US20020004222A1

; GENERAL INFORMATION:  
; APPLICANT: ELISHOURBAGY, NABIL  
; TITLE OF INVENTION: CLONING OF A MONKEY 7TM RECEPTOR (AXOR8)  
; FILE REFERENCE: GP-70673  
; CURRENT APPLICATION NUMBER: US/09/764,556  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: 60/176,852  
; PRIOR FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: MACACA FASCICULARIS  
US-09-764-556-2

Query Match 85.7%; Score 1762; DB 9; Length 384;  
Best Local Similarity 87.4%; Pred. No. 1.9e-160;  
Matches 334; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

QY 12 ATNTSTFSLVNLPHCAHATSPFNFSYSDYDMPDDEEDVTNSRTFFAIVIGMALVG 71  
DB 3 AQNGTSTFAPNFPQDQDASSLSFNSYDGYDLPDDEEDVTNSRTFFAIVIGMALG 62  
QY 72 IMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSWE 131  
DB 63 IMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVRLSWE 122  
QY 132 HGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTATGLIALVMTVSI 191  
DB 123 HGHVLTSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTATGLIALVMTVSI 182  
QY 192 LIAIPSAFYATETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFPIGIEFVGPVVTMLC 251  
DB 183 LIAIPSAFYATETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFPIGIEFVGPVVTMLC 242  
QY 252 YARISRELWFKAVPGFQTEQIRKRLCRKRTVILVLMCILTAIVLVCWAPFYGFTIVRDFEP 311  
DB 243 YARISRELWFKAVPGFQTEQIRKRLCRKRTVILVLMCILTAIVLVCWAPFYGFTIVRDFEP 302  
QY 312 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVYKFKIMLHWRKASVNGKSS 371  
DB 303 TVFVKEKHYLTAFYIVVECIAMNSMINTLCFVTVKNDTVYKFKIMLHWRKASVNGKSS 362  
QY 372 ADDLKTGMPATEEVDICRLK 393  
DB 363 AELDLRTNGVPTATEEVDICRLK 384

## RESULT 13

US-10-132-812-2  
; Sequence 2, Application US/10132812  
; Publication No. US20030059856A1  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Sarau, Henry M.  
; APPLICANT: Slemmon, J. Randall  
; APPLICANT: McNulty, Dean E.  
; APPLICANT: Vawter, Lisa  
; APPLICANT: Foley, James J.  
; TITLE OF INVENTION: Methods Of Screening For Agonists And  
; TITLE OF INVENTION: Agonists Of The Interaction Between The AXOR8 And AXOR52  
; TITLE OF INVENTION: Receptors And Ligands Thereof  
; FILE REFERENCE: PSI256  
; CURRENT APPLICATION NUMBER: US/10/132,812  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: 60/286,234  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 384

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: TYPE: PRT
: ORGANISM: Cercopithecus aethiops
US-10-132-812-2

Query Match      85.7%; Score 1762; DB 15; Length 384;
Best Local Similarity 87.4%; Pred. No. 1.9e-160;
Matches 334; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

QY 12 ATNTSTFSLNPHGAHATSPFPNFSYSDYDMPLEDEDTNSRTFFAAKIVIGNALVG 71
Db 3 AQNGNTSFAPNFPQDQDSSLSNFSGYDYLDPNDEDEMTKTRFFAAKIVIGNALAG 62
QY 72 IMLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 131
Db 63 IMLVCGIGNFVFAALTRYKKRLNLTNLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 122
QY 132 HGHVLTCTSVNLTSLYVSTNALLAIAIDRYLAIVHPLRPMKQATATGLIALVWTYSI 191
Db 123 HGHVLCASVNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPMNTQTASFLIALVWVSI 182
QY 192 LIAIPSAFTTETVLVIVKQKIFCGQIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLC 251
Db 183 LIAIPSAFTATETVLVIVKQKIFCGQIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLC 242
QY 252 YARISRELWFKAVPGFQTEQIRKRLCRRTVLVLMCILTAYVLCWAPFYGFTIVRDFP 311
Db 243 YARISRELWFKAVPGFQTEQIRKRLCRRTVLVLMCILTAYVLCWAPFYGFTIVRDFP 302
QY 312 TVFVKEKHYLTATYVVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLHWKASYNGGKS 371
Db 303 TVFVKEKHYLTATYVVECIAMNSMINTVCFVTVKNTMKYFKKMLLHWRSQSGKS 362
QY 372 ADLDTKTIGMPATEEVDICRLK 393
Db 363 AELDLRTNGVPATEEVDICRLK 384

RESULT 14
US-10-220-289-5
: Sequence 5, Application US/10220289
: Publication No. US20030104435A1
: GENERAL INFORMATION:
: APPLICANT: Bayer AG
: TITLE OF INVENTION: REGULATION OF HUMAN SUBSTANCE P-LIKE G PROTEIN-COUPLED
: FILE REFERENCE: LIA010 Foreign Countries
: CURRENT APPLICATION NUMBER: US/10/220,289
: PRIOR FILING DATE: 2002-09-11
: PRIOR APPLICATION NUMBER: US 60/189,972
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 5
: LENGTH: 385
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-220-289-5

Query Match      85.48; Score 1755.5; DB 15; Length 385;
Best Local Similarity 87.24; Pred. No. 7.9e-160;
Matches 334; Conservative 20; Mismatches 28; Indels 1; Gaps 1;

QY 12 ATNTSTFSLNPHGAHATSPFPNFSYSDYDMPLEDEDTNSRTFFAAKIVIGNALVG 71
Db 3 AQNGNTSFAPNFPQDQDSSLSNFSGYDYLDPNDEDEMTKTRFFAAKIVIGNALAG 62
QY 72 IMLVCGIGNFIFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 131
Db 63 IMLVCGIGNFVFAALTRYKKRLNLTNLLIANLAISDFLVAIVCCPFENDYVYVRLSWE 122
QY 132 HGHVLTCTSVNLTSLYVSTNALLAIAIDR-YLAIVHPLRPMKQATATGLIALVWVSI 190
Db 123 HGHVLCASVNYLRTSVLYSTNALLAIAIDR-LAIAIDRLYLAIHVLKPRMNYQTASFLIALVWVSI 182

Query Match      82.94; Score 1703; DB 15; Length 355;
Best Local Similarity 90.14; Pred. No. 7.6e-155;
Matches 320; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 39 YSDYDMPLEDEDTNSRTFFAAKIVIGNALVGMVCGIGNFIFIAALVRYKKRLNLTN 98
Db 1 YGDYDLPNDEDEMTKTRFFAAKIVIGIALAGIMLVCGIGNFVFAALTRYKKRLNLTN 60
QY 99 LLIANLAISDFLVAIVCCPFENDYVYVRLSWEHGHVLTCTSVNLTSLYVSTNALLAI 158
Db 61 LLIANLAISDFLVAIVCCPFENDYVYVRLSWEHGHVLTCTSVNLTSLYVSTNALLAI 120
QY 159 AIDRYLAIVHPLRPMKQATATGLIALVWVSIILIAISATFTTETVLVIVKQKIFCG 218
Db 121 AIDRYLAIVHPLRPMNTQTASFLIALVWVSIILIAISATFTTETVLVIVKQKIFCG 180
QY 219 QIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLCYARISRELWFKAVPGFQTEQIRKRL 278
Db 181 QIWPVDQQLYKSYFLIFGIEFVGVPVVTMTLCYARISRELWFKAVPGFQTEQIRKRL 240
QY 279 RRKTVLVLMCILTAYVLCWAPFYGFTIVRDFPPTVFVEKHYLTAFYIVECIAMNSMIN 338
Db 241 RRKTVLVLMCILTAYVLCWAPFYGFTIVRDFPPTVFVEKHYLTAFYIVECIAMNSMIN 300
QY 339 TLCFTVTVKNDTVKYFKKIMLLHWKASYNGGSSADLDTKTIGMPATEEVDICRLK 393
Db 301 TVCFVTVKNTMKYFKKMLLHWRSQSGKSADLDTKTIGMPATEEVDICRLK 355

Search completed: October 7, 2003, 10:01:54
Job time : 69 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:48:57 ; Search time 44 Seconds  
(without alignments)  
1417.717 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTWGEMDNDATNTSTSL.....LDLKTIGMPATEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                   |
|------------|-------|-------------|--------|----|-------------------------------|
| 1          | 2055  | 100.0       | 393    | 22 | AAG62854 Amino acid sequenc   |
| 2          | 2055  | 100.0       | 393    | 22 | AAG64121 Human G protein-co   |
| 3          | 2055  | 100.0       | 393    | 22 | ABP81752 Human G protein-co   |
| 4          | 2055  | 100.0       | 393    | 23 | ABG94396 Human GPCR protein   |
| 5          | 2055  | 100.0       | 393    | 23 | ABG99157 Rat ZAQ protein.     |
| 6          | 2055  | 100.0       | 393    | 23 | ABG99157 Human physiologica   |
| 7          | 2055  | 100.0       | 393    | 23 | AAQ15524 Human ZAQ G protei   |
| 8          | 2055  | 100.0       | 393    | 23 | ABG06955 Human ZAQ protein    |
| 9          | 2035  | 99.0        | 389    | 21 | AAB03625 Human ZAQ protein co |

|    |        |      |     |    |          |                    |
|----|--------|------|-----|----|----------|--------------------|
| 10 | 2035   | 99.0 | 389 | 22 | AAG62855 | Amino acid sequenc |
| 11 | 2035   | 99.0 | 389 | 24 | ABG76082 | Human G-protein co |
| 12 | 2035   | 99.0 | 389 | 24 | ABP81752 | Human G protein-co |
| 13 | 1924   | 93.6 | 382 | 23 | ABP76184 | Human G-protein co |
| 14 | 1767   | 86.0 | 393 | 23 | ABG94403 | Rat GPCR protein r |
| 15 | 1767   | 86.0 | 393 | 23 | ABG99158 | Rat rZAQ1 protein. |
| 16 | 1767   | 86.0 | 393 | 23 | ABG06953 | Rat rZAQ1 G protei |
| 17 | 1767   | 86.0 | 393 | 23 | ABG06953 | Rat G protein-coup |
| 18 | 1766   | 85.9 | 384 | 19 | AAW79258 | Human G protein co |
| 19 | 1766   | 85.9 | 384 | 22 | AAU04362 | Human GPCR related |
| 20 | 1766   | 85.9 | 384 | 23 | ABG94405 | Human GPCR related |
| 21 | 1766   | 85.9 | 384 | 23 | ABG99161 | Human 15E. Homo s  |
| 22 | 1766   | 85.9 | 384 | 23 | ABG06311 | Human 15E. Homo s  |
| 23 | 1764   | 85.8 | 393 | 23 | ABG94406 | Mouse GPCR related |
| 24 | 1764   | 85.8 | 393 | 23 | ABG99162 | Mouse GPCR73. Mus  |
| 25 | 1764   | 85.8 | 393 | 23 | ABG06314 | Mouse G protein-co |
| 26 | 1762   | 85.7 | 384 | 22 | AAU04635 | Monkey seven trans |
| 27 | 1755.5 | 85.4 | 385 | 22 | AAG78344 | Neuropeptide Y G p |
| 28 | 1755.5 | 85.4 | 385 | 22 | AAG78505 | Human mature SP-GP |
| 29 | 1715.5 | 83.5 | 421 | 23 | ABG94404 | Rat GPCR protein r |
| 30 | 1715.5 | 83.5 | 421 | 23 | ABG99159 | Rat rZAQ2 protein  |
| 31 | 1715.5 | 83.5 | 421 | 23 | ABG06954 | Rat rZAQ2 G protei |
| 32 | 1715.5 | 83.5 | 421 | 23 | ABG06313 | Rat G protein-coup |
| 33 | 1705   | 83.0 | 630 | 23 | AAE18651 | Human G-protein co |
| 34 | 1699.5 | 82.7 | 381 | 19 | AAW79259 | Mouse GPCR related |
| 35 | 1699.5 | 82.7 | 381 | 23 | ABG94407 | Mouse G protein co |
| 36 | 1699.5 | 82.7 | 381 | 23 | ABG99163 | Mouse GPCR related |
| 37 | 1699.5 | 82.7 | 381 | 23 | ABG06315 | Mouse M15E. Mus a  |
| 38 | 1665.5 | 81.0 | 988 | 22 | ABG18888 | Mouse G protein-co |
| 39 | 1114   | 54.2 | 249 | 22 | ABG07211 | Novel human diagno |
| 40 | 1109   | 54.0 | 231 | 22 | AAG78343 | Neuropeptide Y G p |
| 41 | 1109   | 54.0 | 231 | 22 | AAG78504 | Human SP-GPCR exon |
| 42 | 1042   | 50.7 | 207 | 22 | AAG80945 | Human nGPCR34 #1.  |
| 43 | 1042   | 50.7 | 207 | 23 | ABG93763 | Human G protein-co |
| 44 | 799    | 38.9 | 217 | 22 | AAG62847 | Amino acid sequenc |
| 45 | 657    | 32.0 | 153 | 22 | AAG78342 | Neuropeptide Y G p |

#### ALIGNMENTS

RESULT 1  
AAG62854  
ID AAG62854 standard; Protein; 393 AA.

XX AC

XX AC

XX AC

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of a G-protein coupled receptor.

XX Human; G-protein coupled receptor; GPCR; thyroid disorder;  
KW thyrotoxicosis; myxedema; renal failure; inflammatory condition;  
KW Crohn's disease; arthritis; autoimmune disorder; stroke; migraine;  
KW central nervous system disorder; pain; psychotic disorder;  
KW anxiety disorder; post-traumatic-stress disorder; mania depression;  
KW bipolar disorder; dementia; severe mental retardation;  
KW Huntington's disease; degenerative disorder; Parkinson's;  
KW infection; metabolic disorder; cardiovascular disease;  
KW diabetes; obesity; anorexia; hypotension; hypertension; thrombosis;  
KW myocardial infarction; atherosclerosis; proliferative disease; cancer;  
KW hyperproliferative disorder; psoriasis; prostate hyperplasia;  
KW hormonal disorder; polycystic ovarian syndrome.

XX Homo sapiens.

OS WO200148015-A2.

PN 05-JUL-2001.

PD 28-DEC-2000; 2000WO-US35456.

XX

PR 28-DEC-1999; 99US-0173339.  
 PR 23-FEB-2000; 2000US-0184305.  
 PR 13-MAR-2000; 2000US-0188880.  
 PR 27-APR-2000; 2000US-0200534.  
 PR 20-JUL-2000; 2000US-0219492.  
 PR 11-AUG-2000; 2000US-0224321.  
 PR 09-OCT-2000; 2000US-0239062.  
 XX (PHAA ) PHARMACIA & UPJOHN CO.

XX Lind P, Parodi LA, Lindberg E, Vogeli G, Wood LS, Hiebsch RR;  
 PI Ruff V;  
 XX

DR WPI: 2001-441707/47.  
 DR N-PSDB; AAH42183.

XX G-protein coupled receptor (GPCR-x) nucleic acids and polypeptides  
 PT encoded by them, useful for treating neurological and psychiatric  
 PT disorders such as severe mental retardation, manic depression and  
 PT dementia -

XX Example 1; Page 87; 175pp; English.

XX The present sequence represents human G-protein coupled receptor (GPCR).  
 CC GPCRs may be used in the prevention, treatment and diagnosis of diseases  
 CC associated with inappropriate GPCR expression such as thyroid disorders  
 CC (e.g. thyrotoxicosis, myxedema), renal failure; inflammatory conditions  
 CC (e.g., Crohn's disease); diseases related to cell differentiation and  
 CC homeostasis; rheumatoid arthritis; autoimmune disorders; central  
 CC nervous system (CNS) disorders (e.g., pain including migraine; stroke;  
 CC psychotic and neurological disorders such as anxiety, mental disorder,  
 CC manic depression, generalized anxiety disorder, post-traumatic-stress  
 CC disorder, depression, bipolar disorder, dementia, severe mental  
 CC retardation; Huntington's disease; degenerative disorders such as  
 CC Parkinson's, Alzheimer's; infections such as viral infections caused by  
 CC HIV-1 or HIV-2; metabolic and cardiovascular disease and disorders  
 CC (e.g.: type 2 diabetes, obesity, anorexia, hypotension, hypertension,  
 CC thrombosis, myocardial infarction, atherosclerosis); proliferative  
 CC diseases and cancers and hyperproliferative disorders such as  
 CC psoriasis, prostate hyperplasia); hormonal disorders (male/female  
 CC hormonal replacement, polycystic ovarian syndrome).

XX Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 22; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFYSYSDYDMPDDEDEDVTSRTFFA 60  
 DB 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFYSYSDYDMPDDEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYYVVRQLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 DB 121 DYYVVRQLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 QY 181 GLIALVMTVSLIAIPSAVFTTETVLIVYKSOEKFICGQIWPVDOOLYKYSFLEIFGIE 240  
 DB 181 GLIALVMTVSLIAIPSAVFTTETVLIVYKSOEKFICGQIWPVDOOLYKYSFLEIFGIE 240  
 QY 241 FVGPPVTMTLCYARIISRELWFAVPGFQEQIRKLRRCRRKTVLVLMCLTLYVLCWAPF 300  
 DB 241 FVGPPVTMTLCYARIISRELWFAVPGFQEQIRKLRRCRRKTVLVLMCLTLYVLCWAPF 300  
 QY 301 YGFTIVRDPFPTVFKKHLYLAFYIIVECIANSNMINTLCFTVKNDRVYFKKIMLLH 360  
 DB 301 YGFTIVRDPFPTVFKKHLYLAFYIIVECIANSNMINTLCFTVKNDRVYFKKIMLLH 360  
 QY 361 WKASNGGKSSADLDLKTIGMPATEEVDICRLK 393

DB 361 WKASNGGKSSADLDLKTIGMPATEEVDICRLK 393

RESULT 2

AAG64121  
 ID AAG64121 standard; Protein; 393 AA.

XX AAG64121;

XX 25-SEP-2001 (first entry)

XX Human G protein-coupled receptor GPRV21.

XX Human; guanosine triphosphate binding protein-coupled receptor;  
 KW G-protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;  
 KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;  
 KW Alzheimer's disease; cytostatic; hepatotropic; nootropic;  
 KW neuroprotective; gene therapy; peptide therapy.

XX Homo sapiens.

XX WO200148188-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-JP09408.

XX 28-DEC-1999; 99JP-0375152.

XX 31-MAR-2000; 2000JP-0101339.

XX (HEL1-) HELIX RES INST.

PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;  
 PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;

XX WPI: 2001-425662/45.

XX N-PSDB; AAH73504.

PT New DNA encoding guanosine triphosphate binding protein coupled  
 PT receptors and their expression products for screening potential  
 PT anticancer and nootropic drugs and in diagnosis of these diseases -

XX Claim 1; Page 111-114; 170pp; Japanese.

XX The invention relates to nine human guanosine triphosphate binding  
 CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,  
 CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the  
 CC genes encoding them. These genes and proteins and antibodies against  
 CC the protein are useful in the treatment, prevention, diagnosis and  
 CC investigation of diseases associated with G protein-coupled receptors,  
 CC including cancer, cirrhosis of the liver and Alzheimer's disease.  
 CC The present sequence is a G protein-coupled receptor of the invention.

XX Sequence 393 AA;

Query Match 100.0%; Score 2055; DB 22; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFYSYSDYDMPDDEDEDVTSRTFFA 60  
 DB 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFYSYSDYDMPDDEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYYVVRQLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 DB 121 DYYVVRQLSWEHGHVLTCTSVNYLRTVSLVSNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 QY 181 GLIALVMTVSLIAIPSAVFTTETVLIVYKSOEKFICGQIWPVDOOLYKYSFLEIFGIE 240

|  |   |                |  |     |
|--|---|----------------|--|-----|
| Db   | 181   | GLIALWTVTSILAI | PSAFTTEVTLVIVKSQKIFCGQWMPVDDQQLYTKSYFLIFGIE        | 240 |
| QY   | 241   | FVGPVVTWTL     | CVARISRELWFKAVPGFQTEQIRKRLRCRRKTVLVLWMLITATVYLCWAF | 300 |
| Db   | 241   | FVGPVVTWTL     | CVARISRELWFKAVPGFQTEQIRKRLRCRRKTVLVLWMLITATVYLCWAF | 300 |
| QY   | 301   | YGFTIVROFF     | FPVFKKHLYTAFYIVVECIAMNSMINTLCFTVTKNDVVKFKKIMLHL    | 360 |
| Db   | 301   | YGFTIVROFF     | FPVFKKHLYTAFYIVVECIAMNSMINTLCFTVTKNDVVKFKKIMLHL    | 360 |
| QY   | 361   | WKASNGKGSSAD   | LDLKTIGMPATEEVDICRLK                               | 393 |
| Db   | 361   | WKASNGKGSSAD   | LDLKTIGMPATEEVDICRLK                               | 393 |
| RESULT 3   |   |                |  |     |
| AAB70143   |   |                |  |     |
| ID   | AAB70143 standard; protein; 393 AA.                                     |                |  |     |
| XX   | AAB70143;   |                |  |     |
| XX   | 29-MAY-2001 (first entry)   |                |  |     |
| DT   | XX  |                |  |     |
| DE   | Human G protein-coupled receptor protein.                               |                |  |     |
| XX   | Human; G protein-coupled receptor protein; neotropic; neuroprotective;  |                |  |     |
| KW   | hypotensive; orexigenic; anti-allergic; anti-anginal; antimicrobial;    |                |  |     |
| KW   | antibacterial; gene therapy; Alzheimer's disease; hypertension;         |                |  |     |
| KW   | anorexia; allergy; angina pectoris; infection; MSRA;                    |                |  |     |
| KW   | multiple resistant Staphylococcus aureus.                               |                |  |     |
| XX   | XX  |                |  |     |
| OS   | Homo sapiens.   |                |  |     |
| XX   | XX  |                |  |     |
| XX   | WO200116309-A1.   |                |  |     |
| PN   | XX  |                |  |     |
| XX   | 08-MAR-2001.  |                |  |     |
| PD   | XX  |                |  |     |
| XX   | 24-AUG-2000; 2000WO-JP05685.  |                |  |     |
| PF   | XX  |                |  |     |
| XX   | 27-AUG-1999; 99JP-0241531.  |                |  |     |
| PR   | 18-JUL-2000; 2000JP-0217474.  |                |  |     |
| PR   | XX  |                |  |     |
| PA   | (TAKE ) TAKEDA CHEM IND LTD.  |                |  |     |
| XX   | XX  |                |  |     |
| PI   | Watanabe T, Terao Y, Shintani Y;  |                |  |     |
| PI   | XX  |                |  |     |
| DR   | WPI; 2001-226684/23.  |                |  |     |
| DR   | N-PSDB; AAF79501.   |                |  |     |
| XX   | XX  |                |  |     |
| PT   | New human brain-originated guanosine triphosphate protein-coupled       |                |  |     |
| PT   | receptor protein, its salt and encoded gene, useful in (gene) diagnosis |                |  |     |
| PT   | and development of preventives and remedies for Alzheimer's disease,    |                |  |     |
| PT   | hypertension and anorexia   |                |  |     |
| XX   | XX  |                |  |     |
| PS   | Cialm 1; Fig 1-3; 119pp; Japanese.                                      |                |  |     |
| XX   | XX  |                |  |     |
| CC   | The present sequence is provided in a specification relating to a       |                |  |     |
| CC   | protein or its salt with an amino acid sequence identical or            |                |  |     |
| CC   | substantially similar to a fully defined sequence of 393 amino acids as |                |  |     |
| CC   | given in the specification. The protein is useful in gene diagnosis and |                |  |     |
| CC   | development of preventives and remedies for diseases associated with    |                |  |     |
| CC   | dysfunction of the protein, e.g. Alzheimer's disease, hypertension,     |                |  |     |
| CC   | anorexia, allergy, angina pectoris and infections (e.g. multiple        |                |  |     |
| CC   | resistant Staphylococcus aureus. The proteins and DNA encoding the      |                |  |     |
| CC   | proteins are also useful for the treatment of these diseases by gene    |                |  |     |
| CC   | therapy.  |                |  |     |
| XX   | XX  |                |  |     |
| SQ   | Sequence 393 AA;  |                |  |     |
| Query Match 100.0%; Score 2055; DB 22; Length 393;           |   |                |  |     |
| Best Local Similarity 100.0%; Pred. No. 3.7e-227;            |   |                |  |     |
| Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |                |  |     |

CC for their ability to modify the binding of G-protein coupled receptor  
 CC (GPCR) protein ZAQ and related proteins (human ZAQ, human ZAQ1,  
 CC rat ZAQ1 (rZAQ1), rZAQ2, human and mouse ISE (mISE) receptor, and  
 CC mouse GPR73) to their ligands (the mature form of human, mouse or rat  
 CC Bv8 protein). The receptor protein and ligand are contacted in the  
 CC presence or absence of the test compound. The compounds are useful  
 CC in a drug composition for the treatment, and prevention of digestive  
 CC and central nervous system (CNS) disorders, including bowel  
 CC inflammation, diarrhoea, constipation, food absorption disorders,  
 CC Alzheimer's disease, Parkinson's disease and schizophrenia.  
 CC The present sequence represents a GPCR or related protein.  
 XX  
 SQ Sequence 393 AA;  
 Query Match 100.0%; Score 2055; DB 23; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPDLEDEDVTSRTFFA 60  
 DB 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPDLEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYVVVQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 DB 121 DYVVVQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 QY 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKQKIFCGQIWPVDQQLYKSYFLFIGIE 240  
 DB 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKQKIFCGQIWPVDQQLYKSYFLFIGIE 240  
 QY 241 FVGPVVMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLMCLITAYVLCWAPF 300  
 DB 241 FVGPVVMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLMCLITAYVLCWAPF 300  
 QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLH 360  
 DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLH 360  
 QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393  
 DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393  
 RESULT 5  
 ABB99157  
 ID ABB99157 standard; Protein; 393 AA.  
 XX  
 AC ABB99157;  
 DT 15-NOV-2002 (first entry)  
 DE Rat ZAQ protein.  
 XX  
 KW Rat; physiological; G protein-coupled receptor; ZAQ; antidiarrheic;  
 KW laxative; anti-inflammatory; digestive disease; diarrhoea; constipation;  
 KW colitis; gene therapy.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200262996-A1.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 01-FEB-2002; 2002WO-JP00837.  
 XX  
 PR 02-FEB-2001; 2001JP-0026798.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX

PI Ohtaki T, Masuda Y, Takatsu Y;  
 XX WPI; 2002-627554/67.  
 DR N-PSDB; ABQ79083, ABQ79084.  
 XX  
 PT Physiologically-active brain-originated G protein-coupled receptor  
 PT peptide ZAQ and encoding DNA, useful for developing drugs to treat  
 PT digestive diseases e.g. diarrhoea, constipation and colitis, including  
 PT gene therapy -  
 XX  
 FS Claim 16; Fig 1-3; 184pp; Japanese.  
 XX  
 CC The invention relates to a novel physiologically-active brain-originated  
 CC G protein-coupled receptor peptide designated ZAQ. The proteins of the  
 CC invention have antidiarrheic, laxative, and anti-inflammatory activity.  
 CC The DNA and encoded protein are useful for developing drugs for the  
 CC treatment of diseases of the digestive organs e.g. diarrhoea,  
 CC constipation and colitis. The polynucleotides may have a use in gene  
 CC therapy. The sequence represents a rat ZAQ protein of the invention.  
 XX  
 SQ Sequence 393 AA;  
 Query Match 100.0%; Score 2055; DB 23; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPDLEDEDVTSRTFFA 60  
 DB 1 METTMGFMDNATNTSTSLVLPNPHGHAHATSPFPNFSDYDMPDLEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYVVVQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 DB 121 DYVVVQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCOAT 180  
 QY 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKQKIFCGQIWPVDQQLYKSYFLFIGIE 240  
 DB 181 GLIALVWTVSILIAIPSAFTTETVLVIVKSKQKIFCGQIWPVDQQLYKSYFLFIGIE 240  
 QY 241 FVGPVVMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLMCLITAYVLCWAPF 300  
 DB 241 FVGPVVMTLCYARISRELWFKAVPGFQTEOIRKRLCRKRTVLMCLITAYVLCWAPF 300  
 QY 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLH 360  
 DB 301 YGFTIVRDFPFTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKFKKIMLH 360  
 QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393  
 DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393  
 RESULT 6  
 AA015524  
 ID AA015524 standard; Protein; 393 AA.  
 XX  
 AC AA015524;  
 DT 24-OCT-2002 (first entry)  
 DE Human physiologically-active ZAQ ligand-related protein 1.  
 XX  
 KW Human; ZAQ ligand; physiologically-active ZAQ ligand;  
 KW digestive disease; colitis; diarrhoea.  
 OS Homo sapiens.  
 XX  
 PN WO200257443-A1.  
 XX  
 PD 25-JUL-2002.

XX 21-JAN-2002; 2002WO-JP00378.  
 XX  
 PR 22-JAN-2001; 2001JP-0013027.  
 PR 17-MAY-2001; 2001JP-0147759.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PA Yamada T, Suenaga M, Nishimura O;  
 PI WPI; 2002-566801/60.  
 XX  
 DR Industrial production of physiologically-active ZAQ ligand by  
 XX expressing in transformant prokaryote and refolding in redox buffer,  
 PT for use in preventing or treating digestive diseases e.g. colitis and  
 PT diarrhea  
 XX  
 PS Claim 1; Page 66-68; 93pp; Japanese.  
 XX  
 CC The invention comprises a method for producing an active peptide that has  
 CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The  
 CC method of the invention is useful for the production of a  
 CC physiologically-active ZAQ ligand for use in preventing or treating  
 CC digestive diseases (e.g. colitis and diarrhea). The present amino acid  
 CC sequence represents a human physiologically active ZAQ ligand-related  
 CC protein.  
 XX  
 SQ Sequence 393 AA;  
 Query Match 100.0%; Score 2055; DB 23; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60  
 DB 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180  
 DB 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180  
 QY 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKFQIRKRLCRKRKTVLVMCILTAYVLCWAPF 240  
 DB 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKFQIRKRLCRKRKTVLVMCILTAYVLCWAPF 240  
 QY 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTAYVLCWAPF 300  
 DB 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTAYVLCWAPF 300  
 QY 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360  
 DB 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360  
 QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393  
 DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393  
 RESULT 7  
 ID ABB06955 standard; Protein; 393 AA.  
 XX  
 AC ABB06955;  
 XX  
 DT 19-JUN-2002 (first entry)  
 XX  
 DE Human ZAQ G protein-coupled receptor protein SEQ ID NO:12.  
 XX  
 KW Human; rZAQ1; rZAQ2; G protein-coupled receptor; GPCR; antidiarrheic;

KW laxative; drug development; digestive organ disease; colitis; diarrhoea;  
 KW constipation; malabsorption syndrome; diagnosis; gene therapy.  
 XX Homo sapiens.  
 OS  
 PN WO200216607-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 XX 23-AUG-2001; 2001WO-JP07209.  
 XX  
 PR 24-AUG-2000; 2000JP-0253862.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Teraso Y, Shintani Y;  
 XX  
 XX WPI; 2002-269361/31.  
 DR  
 XX Human and rat brain-originated G protein-coupled receptor proteins and  
 XX encoded DNAs, for developing drugs to treat diseases of the digestive  
 PT organs, e.g. colitis, diarrhea, constipation and mal-absorption  
 PT syndrome  
 XX  
 PS Example 1; Page 101-102; 135pp; Japanese.  
 XX  
 CC The present invention describes human and rat brain-originated  
 CC G protein-coupled receptor (GPCR) proteins. The GPCR sequences have  
 CC antidiarrheic and laxative activities. The GPCR sequences can be used  
 CC for developing drugs to treat diseases of the digestive organs,  
 CC e.g. colitis, diarrhoea, constipation and malabsorption syndrome,  
 CC including gene diagnosis and therapy. The present sequence represents  
 CC a human GPCR designated ZAQ, which is given in the present invention.  
 XX  
 SQ Sequence 393 AA;  
 Query Match 100.0%; Score 2055; DB 23; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60  
 DB 1 METTGMFDDNATNTSTSLVNLPHGAHATSPFNFSYSDYDMPDLEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180  
 DB 121 DYYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPMKCQTAT 180  
 QY 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKFQIRKRLCRKRKTVLVMCILTAYVLCWAPF 240  
 DB 181 GLIALVMTVTSILIAIPSAFTTETVLVIVKSOEKFQIRKRLCRKRKTVLVMCILTAYVLCWAPF 240  
 QY 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTAYVLCWAPF 300  
 DB 241 FVGPPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVMCILTAYVLCWAPF 300  
 QY 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360  
 DB 301 YGFTIVRDEFPPTVVKKEHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360  
 QY 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393  
 DB 361 WKASNGKSSADLDLKTIGMPATEEVDICRLK 393  
 RESULT 8  
 ID ABB06303 standard; Protein; 393 AA.  
 XX

AC ABB06303;  
 XX 27-MAY-2002 (first entry)  
 DT Human ZAQ protein sequence SEQ ID NO:1.  
 XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;  
 KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;  
 KW colitis; diarrhoea; constipation; poor-absorption syndrome;  
 KW gene therapy.  
 XX Homo sapiens.  
 OS WO200206483-A1.  
 PN 24-JAN-2002.  
 PD 17-JUL-2001; 2001WO-JP06162.  
 PF 18-JUL-2000; 2000JP-0217442.  
 PR 02-FEB-2001; 2001JP-0026779.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;  
 PI Hinuma S;  
 PI WPI: 2002-188546/24.  
 DR N-PSDB: ABL49615, ABL49616.  
 XX Physiologically-active peptides from cows milk, useful for developing  
 PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases  
 PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by  
 PT gene therapy.  
 XX Claim 14; Page 51-52; 191pp; Japanese.  
 PS The present invention describes a peptide containing an amino acid  
 XX sequence (I) identical to or substantially similar to that of the  
 CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic  
 CC and laxative activities. The peptides and encoding DNAs from the  
 CC present invention are useful for developing drugs to treat digestive  
 CC diseases like colitis, diarrhoea, constipation and poor-absorption  
 CC syndrome, including gene therapy. The physiologically-active cows  
 CC milk-originated peptides are applicable as a specific ligand of  
 CC brain-originated orphan G protein-coupled receptor protein ZAQ.  
 CC ABL49615 to ABB40659 and ABB06303 to ABB06315 represent sequences  
 CC used in the exemplification of the present invention.  
 XX Sequence 393 AA;  
 SQ Query Match 100.0%; Score 2055; DB 23; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-227;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 M E T T G F M D N A T W T S F L S V L N P H G A H A T S P F N F S Y S D Y D M P L D E D E D V T N S R T F F A 60  
 DB 1 M E T T G F M D N A T W T S F L S V L N P H G A H A T S P F N F S Y S D Y D M P L D E D E D V T N S R T F F A 60  
 QY 61 A K I V I G M A L V G I M L V C G I G N F I F I A A L V R Y K K L R N L T N L I A N L A I S D F L V A I V C C P F E M 120  
 DB 61 A K I V I G M A L V G I M L V C G I G N F I F I A A L V R Y K K L R N L T N L I A N L A I S D F L V A I V C C P F E M 120  
 QY 121 D Y Y V V R Q L S W E H G V L C T S V N L R T V S L Y S T N A L L A I A I D R Y L A I V H P L R P M K C O T A T 180  
 DB 121 D Y Y V V R Q L S W E H G V L C T S V N L R T V S L Y S T N A L L A I A I D R Y L A I V H P L R P M K C O T A T 180  
 QY 181 G L I A L W T V S I L I A P S A Y F T T E T V L V I V K S Q E K I F C G Q I W P V D Q Q L Y K S Y F L F I G I E 240  
 DB 181 G L I A L W T V S I L I A P S A Y F T T E T V L V I V K S Q E K I F C G Q I W P V D Q Q L Y K S Y F L F I G I E 240  
 QY 241 F V G P V V T M T L C Y A R I S R E L W F K A V P G F Q T E I R K R L C R R K T V L V L M C I L T A Y V L C W A P F 300  
 DB 241 F V G P V V T M T L C Y A R I S R E L W F K A V P G F Q T E I R K R L C R R K T V L V L M C I L T A Y V L C W A P F 300

Db 241 F V G P V V T M T L C Y A R I S R E L W F K A V P G F Q T E I R K R L C R R K T V L V L M C I L T A Y V L C W A P F 300  
 QY 301 Y G F T I V R D F P P T V F V K E K H Y L T A F Y I V E C T A N S N S M I N T L C F V T V K N D T V K Y F K K I M L L H 360  
 Db 301 Y G F T I V R D F P P T V F V K E K H Y L T A F Y I V E C T A N S N S M I N T L C F V T V K N D T V K Y F K K I M L L H 360  
 QY 361 W K A S Y N G K S S A D L D L K T I G M P A T E E V D C I R L K 393  
 Db 361 W K A S Y N G K S S A D L D L K T I G M P A T E E V D C I R L K 393  
 RESULT 9  
 AAB03625  
 ID AAB03625 standard; Protein; 389 AA.  
 XX AAB03625;  
 AC AAB03625;  
 DT 03-JAN-2001 (first entry)  
 DE Human G-protein coupled receptor fb41a.  
 XX Human; fb41a; G-protein coupled receptor; memory loss; depression;  
 KW anxiety; epilepsy; pain; hypertension; locomotor problems;  
 KW circadian rhythm disorder; eating/body weight disorder;  
 KW sexual/reproductive disorder; nasal congestion; diarrhoea;  
 KW gastrointestinal disorder; cardiovascular disorder.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Domain 58..84 /label= potential\_transmembrane\_region  
 FT Domain 95..117 /label= potential\_transmembrane\_region  
 FT Domain 136..156 /label= potential\_transmembrane\_region  
 FT Domain 175..196 /label= potential\_transmembrane\_region  
 FT Domain 228..249 /label= potential\_transmembrane\_region  
 FT Domain 282..305 /label= potential\_transmembrane\_region  
 FT Domain 319..341 /label= potential\_transmembrane\_region  
 FT Domain /label= potential\_transmembrane\_region  
 WO2000034334-A1.  
 PN 15-JUN-2000.  
 PD 10-DEC-1999; 99WO-US29268.  
 PF 10-DEC-1998; 98US-0210279.  
 PR (SYNA-) SYNAPTIC PHARM CORP.  
 PA Bard JA;  
 PI WPI: 2000-431277/37.  
 DR N-PSDB: AAA53210.  
 XX Novel nucleic acid encoding a mammalian fb41a receptor useful for  
 PT treating hypertension, diabetes, asthma, obesity and gastrointestinal  
 PT disorders.  
 XX Claim 9; Fig 2; 133pp; English.  
 PS The present sequence is the protein sequence for the human fb41a  
 CC G-protein coupled receptor. This protein is a neuroregulator and is  
 CC involved in communication within the nervous system. Its coding sequence  
 CC was isolated by screening a human placental genomic DNA library for  
 CC sequences similar to that encoding APL4. The gene and protein can be  
 CC used to treat the following types of disorder: those involving the  
 CC regulation of steroid hormones, epinephrine release, the

CC gastrointestinal tract, the cardiovascular system, electrolyte  
 CC balance, hypertension, diabetes, respiration, asthma, reproductive  
 CC function, the immune system, endocrine function, the musculoskeletal  
 CC system, visceral innervation, neuroendocrine function, cognition, sensory  
 CC memory, sensory modulation and transmission, motor coordination, sensory  
 CC integration, motor integration, dopaminergic function, appetite,  
 CC obesity, olfaction, sympathetic innervation or migraine.  
 XX Sequence 389 AA;

Query Match 99.0%; Score 2035; DB 21; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-225;  
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 MGFDDNATNTSTFSLVNLPHGAHATSPFNFYSYSDYDMPLEDEDTNSRTFFAAKIV 64  
 Db 1 MGFDDNATNTSTFSLVNLPHGAHATSPFNFYSYSDYDMPLEDEDTNSRTFFAAKIV 60  
 Qy 65 IGMALVIGIMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 124  
 Db 61 IGMALVIGIMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 120  
 Qy 125 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLRPMKOTATGLIA 184  
 Db 121 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLRPMKOTATGLIA 180  
 Qy 185 LVWTVSILIAIPSAFYTTETVLVIVKSOEIKFCQIWPVDQQLYKSYFLFIEFVGP 244  
 Db 181 LVWTVSILIAIPSAFYTTETVLVIVKSOEIKFCQIWPVDQQLYKSYFLFIEFVGP 240  
 Qy 245 VVTMTLCYARISRELKFAVPGFQEQIRKRLCRRTVLVLMCILTAIVLCWAPFYGT 304  
 Db 241 VVTMTLCYARISRELKFAVPGFQEQIRKRLCRRTVLVLMCILTAIVLCWAPFYGT 300  
 Qy 305 IVRDFPTFVKEKHLYTAFYIVCEIAMSNSMINTLCFVTKNDTVYFKKIMLLHWKAS 364  
 Db 301 IVRDFPTFVKEKHLYTAFYIVCEIAMSNSMINTLCFVTKNDTVYFKKIMLLHWKAS 360  
 Qy 365 YNGKSSADLLKTIQMPATEVDCIRLK 393  
 Db 361 YNGKSSADLLKTIQMPATEVDCIRLK 389

RESULT 10  
 AAG62855  
 ID AAG62855 standard; Protein: 389 AA.  
 XX AC AAG62855;  
 XX DT 17-SEP-2001 (first entry)  
 XX DE Amino acid sequence of a G-protein coupled receptor.  
 XX KW Human; G-protein coupled receptor; GPCR; thyroid disorder;  
 KW thyrotoxicosis; myxedema; renal failure; inflammatory condition;  
 KW Crohn's disease; arthritis; autoimmune disorder; stroke; migraine;  
 KW central nervous system disorder; pain; psychotic disorder;  
 KW neurological disorder; anxiety; mental disorder; manic depression;  
 KW anxiety disorder; post-traumatic-stress disorder; depression;  
 KW bipolar disorder; dementia; severe mental retardation;  
 KW Huntington's disease; degenerative disorder; Parkinson's; Alzheimer's;  
 KW infection; metabolic disorder; cardiovascular disease;  
 KW diabetes; obesity; anorexia; hypotension; hypertension; thrombosis;  
 KW myocardial infarction; atherosclerosis; proliferative disease; cancer;  
 KW hyperproliferative disorder; psoriasis; prostate hyperplasia;  
 KW hormonal disorder; polycystic ovarian syndrome.  
 XX OS Homo sapiens.  
 XX PN WO200148015-A2.  
 XX PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35456.  
 XX 28-DEC-1999; 99US-0173339.  
 PR 23-FEB-2000; 2000US-0184305.  
 PR 13-MAR-2000; 2000US-0188880.  
 PR 27-APR-2000; 2000US-0200534.  
 PR 20-JUL-2000; 2000US-0219492.  
 PR 11-AUG-2000; 2000US-0224321.  
 PR 09-OCT-2000; 2000US-0239062.  
 XX (PHAA ) PHARMACIA & UPJOHN CO.  
 PA Lind P, Parodi LA, Lindberg E, Vogeli G, Wood LS, Hiebsch RR;  
 PI Ruff V;  
 XX WPI; 2001-441707/47.  
 DR N-PSDB; AAH42183.  
 XX G-protein coupled receptor (GPCR-x) nucleic acids and polypeptides  
 PT encoded by them, useful for treating neurological and psychiatric  
 PT disorders such as severe mental retardation, manic depression and  
 PT dementia -  
 XX Example 1; Page 87; 175pp; English.  
 PS The present sequence represents human G-protein coupled receptor (GPCR).  
 CC GPCRs may be used in the prevention, treatment and diagnosis of diseases  
 CC associated with inappropriate GPCR expression such as thyroid disorders  
 CC (e.g. thyrotoxicosis, myxedema), renal failure; inflammatory conditions  
 CC (e.g., Crohn's disease); diseases related to cell differentiation and  
 CC homeostasis; rheumatoid arthritis; autoimmune disorders; central  
 CC nervous system (CNS) disorders (e.g., pain including migraine; stroke;  
 CC psychotic and neurological disorders such as anxiety, mental disorder,  
 CC manic depression, generalized anxiety disorder, post-traumatic-stress  
 CC disorder, depression, bipolar disorder, dementia, severe mental  
 CC retardation; Huntington's disease; degenerative disorders such as  
 CC Parkinson's, Alzheimer's; infections such as viral infections caused by  
 CC HIV-1 or HIV-2; metabolic and cardiovascular disease and disorders  
 CC (e.g., type 2 diabetes, obesity, anorexia, hypotension, hypertension,  
 CC thrombosis, myocardial infarction, atherosclerosis); proliferative  
 CC diseases and cancers and hyperproliferative disorders such as  
 CC psoriasis, prostate hyperplasia); hormonal disorders (male/female  
 CC hormonal replacement, polycystic ovarian syndrome).  
 XX SQ Sequence 389 AA;

Query Match 99.0%; Score 2035; DB 22; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-225;  
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 MGFDDNATNTSTFSLVNLPHGAHATSPFNFYSYSDYDMPLEDEDTNSRTFFAAKIV 64  
 Db 1 MGFDDNATNTSTFSLVNLPHGAHATSPFNFYSYSDYDMPLEDEDTNSRTFFAAKIV 60  
 Qy 65 IGMALVIGIMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 124  
 Db 61 IGMALVIGIMLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYV 120  
 Qy 125 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLRPMKOTATGLIA 184  
 Db 121 VROLSEHGHLVCTSVNYLRTVSVLTNALLAIAIDRYLAIVHPLRPMKOTATGLIA 180  
 Qy 185 LVWTVSILIAIPSAFYTTETVLVIVKSOEIKFCQIWPVDQQLYKSYFLFIEFVGP 244  
 Db 181 LVWTVSILIAIPSAFYTTETVLVIVKSOEIKFCQIWPVDQQLYKSYFLFIEFVGP 240  
 Qy 245 VVTMTLCYARISRELKFAVPGFQEQIRKRLCRRTVLVLMCILTAIVLCWAPFYGT 304  
 Db 241 VVTMTLCYARISRELKFAVPGFQEQIRKRLCRRTVLVLMCILTAIVLCWAPFYGT 300  
 Qy 305 IVRDFPTFVKEKHLYTAFYIVCEIAMSNSMINTLCFVTKNDTVYFKKIMLLHWKAS 364  
 Db 301 IVRDFPTFVKEKHLYTAFYIVCEIAMSNSMINTLCFVTKNDTVYFKKIMLLHWKAS 360



QY 365 YNGKSSADLDLKTIGMPATEVDCIRLK 393  
DB 361 YNGKSSADLDLKTIGMPATEVDCIRLK 389  
RESULT 11  
ID ABG76082 standard; Protein; 389 AA.  
XX  
AC ABG76082;  
XX  
DT 09-MAY-2003 (first entry)  
XX  
DE Human G-protein coupled receptor fb41a.  
XX  
KW Human; fb41a; GPCR; G-protein coupled receptor; immune disorder;  
KW fb41a associated disorder; steroid hormone regulation; appetite;  
KW epinephrine release; gastrointestinal disorder; reproductive disorder;  
KW endocrine disorder; musculoskeletal disorder; visceral innervation  
KW neuroendocrine disorder; cognitive disorder; motor coordination;  
KW memory; sensory modulation; sensory transmission; sensory integration;  
KW motor integration; dopaminergic function; olfaction; hypertension;  
KW sympathetic innervation; cardiovascular disorder; respiratory disorder;  
KW electrolyte balance disorder; diabetes; asthma; migraine.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 4..389  
FT /label= Truncated\_fb41a  
FT /note= "This is the truncated form of fb41a  
FT encoded by ABX11940".  
XX  
PN US2002165380-A1.  
XX  
PD 07-NOV-2002...  
XX  
PF 09-AUG-2001; 2001US-0925922.  
XX  
PR 10-DEC-1998; 98US-0210279.  
XX  
PA (BARD/) BARD J A.  
PI Bard JA;  
XX  
XX WPI; 2003-288148/28.  
DR N-PSDB; ABX11940.  
XX  
PT New isolated human fb41a receptor nucleic acid, useful for the  
PT diagnosis, prevention or treatment of disorders with aberrant  
PT expression or activity of the fb41a receptor protein, such as  
PT hypertension, diabetes, asthma and migraine.  
XX  
PS Claim 9; Fig 2; 40pp; English.  
XX  
CC The invention relates to an isolated nucleic acid encoding a mammalian  
CC G-protein coupled receptor, fb41a. The methods and compositions of the  
CC present invention are useful for the diagnosis, prevention and/or  
CC treatment of disorders associated with aberrant expression or activity of  
CC the fb41a receptor protein, such as regulation of steroid hormone,  
CC epinephrine release, gastrointestinal, reproductive, immune, endocrine,  
CC musculoskeletal, visceral innervation, neuroendocrine, cognitive, motor  
CC coordination, memory, sensory modulation, sensory or motor integration,  
CC dopaminergic function, appetite, sensory transmission, olfaction,  
CC sympathetic innervation, cardiovascular, respiratory and electrolyte  
CC balance disorders, hypertension, diabetes, asthma and migraine. The  
CC present sequence represents the amino acid sequence of the human  
CC G-protein coupled receptor fb41a.  
XX  
SQ Sequence 389 AA;

Query Match 99.0%; Score 2035; DB 24; Length 389;

Best Local Similarity 100.0%; Pred. No. 7.3e-225;  
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 MGFMDNATNTSTSLVLPNGAHATSPFFNFSDYDMPDLEDESDVNSRTFFFAKIV 64  
DB 1 MGFMDNATNTSTSLVLPNGAHATSPFFNFSDYDMPDLEDESDVNSRTFFFAKIV 60  
QY 65 IGMALVGIMLVCCGIGNFIFIAALVRYKKLNLIANLAIISDELVAIVCCPFENDYV 124  
DB 61 IGMALVGIMLVCCGIGNFIFIAALVRYKKLNLIANLAIISDELVAIVCCPFENDYV 120  
QY 125 VROLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIYHPLRPMKCTATGLIA 184  
DB 121 VROLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIYHPLRPMKCTATGLIA 180  
QY 185 LVMTVSTLIAIPSAFTTETVLVIVKSOEIKFGQWPDQOQLYKSYFLFIFGIEFVGP 244  
DB 181 LVMTVSTLIAIPSAFTTETVLVIVKSOEIKFGQWPDQOQLYKSYFLFIFGIEFVGP 240  
QY 245 VVTMTLCYARISRELWFKAYPGFQTEQIRKRLRCRRKTVLVMCILTAYVLCWAPFGFT 304  
DB 241 VVTMTLCYARISRELWFKAYPGFQTEQIRKRLRCRRKTVLVMCILTAYVLCWAPFGFT 300  
QY 305 IVRDFFTVFKKHYLTAFYIIVECIAMSNMINTLCFVTYKNDTVKYFKKIMLHWKAS 364  
DB 301 IVRDFFTVFKKHYLTAFYIIVECIAMSNMINTLCFVTYKNDTVKYFKKIMLHWKAS 360  
QY 365 YNGKSSADLDLKTIGMPATEVDCIRLK 393  
DB 361 YNGKSSADLDLKTIGMPATEVDCIRLK 389  
RESULT 12  
ABP81752  
ID ABP81752 standard; Protein; 389 AA.  
XX  
AC ABP81752;  
XX  
DT 04-MAR-2003 (first entry)  
XX  
DE Human G protein-coupled receptor hFB41A protein SEQ ID NO:678.  
XX  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
XX  
OS Homo sapiens.  
XX  
PN WO200261087-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 19-DEC-2001; 2001WO-US50107.  
XX  
PR 19-DEC-2000; 2000US-257144P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
PI Burmer GC, Roush CL, Brown JP;  
XX  
XX WPI; 2003-046718/04.  
DR N-PSDB; ABZ42597.  
XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating

PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases -  
 PS Disclosure; Fig 1; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (1) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related diseases, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABP242523 to ABP242869 encode  
 CC GPCR proteins given in ABP1675 to ABP82018, which are used in the  
 CC exemplification of the present invention.

XX Sequence 389 AA;

Query Match 99.0%; Score 2035; DB 24; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-225;  
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 MGFMDDNATNTSTFSLVLPNGAHATSPFPNFYSYDMPDDEDEVTNSRTFFAAKIV 64  
 DB 1 MGFMDDNATNTSTFSLVLPNGAHATSPFPNFYSYDMPDDEDEVTNSRTFFAAKIV 60  
 QY 65 IGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEMDYV 124  
 DB 61 IGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEMDYV 120  
 QY 125 VRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQOTATGLIA 184  
 DB 121 VRQLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQOTATGLIA 180  
 QY 185 LVWTVSILIAIPSAFYFTETVLVIVKSGEIKFCQIWPVDQOLYKSYFLFIEFVGP 244  
 DB 181 LVWTVSILIAIPSAFYFTETVLVIVKSGEIKFCQIWPVDQOLYKSYFLFIEFVGP 240  
 QY 245 VVTMLCYARISRELKFAVPGFQTEIRKRLCRRTKTLVLMCILTAIVLCHAPFYGYFT 304  
 DB 241 VVTMLCYARISRELKFAVPGFQTEIRKRLCRRTKTLVLMCILTAIVLCHAPFYGYFT 300  
 QY 305 IVRDFFFTVFKEKHLYTAFYIVECIAHNSMINTLCFVTVKNDTVYFKKIMLLHWKAS 364  
 DB 301 IVRDFFFTVFKEKHLYTAFYIVECIAHNSMINTLCFVTVKNDTVYFKKIMLLHWKAS 360  
 QY 365 YNGKSSADLDLKTIGMPATEYDCIRLK 393  
 DB 361 YNGKSSADLDLKTIGMPATEYDCIRLK 389

RESULT 13

ABB76184

ID ABB76184 standard; Protein; 382 AA.

XX

AC ABB76184;

XX

DT 05-AUG-2002 (first entry)

XX Human G-protein coupled receptor AXOR52.  
 DE  
 XX  
 KW AXOR52; human; G-protein coupled receptor; receptor; viroclide;  
 KW anti-HIV; analgesic; cytostatic; antidiabetic; osteopathic;  
 KW antiparkinsonian; cardiac; antiulcer; antiallergic;  
 KW tranquilizer; antidepressant; hypotensive; hypertensive;  
 KW gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN GB2368065-A.  
 XX  
 XX 24-APR-2002.  
 XX  
 XX 09-JUL-2001; 2001GB-0016714.  
 XX  
 XX 10-JUL-2000; 2000US-0612772.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Elshourbagy N, Shabon U, Michalovich D, Gattu M, Duckworth M;  
 PI  
 XX WPI; 2002-419117/45.  
 XX  
 XX N-PSDB; ABL57089.  
 XX  
 XX New human AXOR52 receptor polypeptide, useful for treatment and  
 PT diagnosis of e.g. viral infections, also related nucleic acid,  
 PT antibodies and modulators -  
 PT  
 XX  
 PS Claim 1; Page 30-31; 35pp; English.  
 XX  
 CC The present sequence is the protein sequence for human AXOR52, a  
 CC novel NPX-like G-protein coupled receptor. The invention provides  
 CC AXOR52 polypeptides and polynucleotides (see ABL57089), expression  
 CC vectors, host cells, processes for producing the host cells and  
 CC polypeptides, and antibodies immunospecific for the AXOR52  
 CC polypeptides. The polypeptides and polynucleotides may be useful  
 CC for treatment of bacterial, fungal, protozoan and viral infections  
 CC (particularly HIV-1 or HIV-2), pain, cancer, diabetes, obesity,  
 CC anorexia, bulimia, asthma, Parkinson's disease, acute heart  
 CC failure, hypotension, hypertension, urinary retention,  
 CC osteoporosis, angina pectoris, myocardial infarction, stroke,  
 CC ulcers, asthma, allergy, benign prostatic hypertrophy, migraine,  
 CC vomiting, psychotic and neurological disorders including anxiety,  
 CC schizophrenia, manic depression, delirium, dementia, and severe  
 CC mental retardation, and dyskinesias such as Huntington's disease  
 CC and Gilles de la Tourette's syndrome. They are also useful for  
 CC identifying agonists and antagonists, in diagnostic assays for  
 CC detecting diseases associated with inappropriate AXOR52 activity or  
 CC levels, and in vaccines.

XX Sequence 382 AA;

Query Match 93.6%; Score 1924; DB 23; Length 382;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-212;  
 Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METTMGPMDDNATNTSTFSLVLPNGAHATSPFPNFYSYDMPDDEDEVTNSRTFFA 60  
 DB 1 METTMGPMDDNATNTSTFSLVLPNGAHATSPFPNFYSYDMPDDEDEVTNSRTFFA 60  
 QY 61 AKIVIGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEM 120  
 DB 61 AKIVIGMALVIGMLVCGIGNFIFIAALVRYKKLNLTNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYTIVVROLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQOTAT 180  
 DB 121 DYTIVVROLSWEHGHVLCSTVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQOTAT 180  
 QY 181 GLIALVWTVSILIAIPSAFYFTETVLVIVKSGEIKFCQIWPVDQOLYKSYFLFIEGIE 240  
 DB 181 GLIALVWTVSILIAIPSAFYFTETVLVIVKSGEIKFCQIWPVDQOLYKSYFLFIEGIE 240

Db 181 GLIALVMTVSYLIIAIPSAFYTTTETVLIVIVKSOEIKFCGQWPDQOLYKYSFLFPIGIE 240  
 QY 241 FVGPPVMTLTCVARIISRELWFKAVPGFQEQIRKRLRCRKTVLVLMCLITAYVLCWAPF 300  
 Db 241 FVGPPVMTLTCVARIISRELWFKAVPGFQEQIRKRLRCRKTVLVLMCLITAYVLCWAPF 300  
 QY 301 YGFTIVRDFPPTVFKVKEHYLTAFAIVECIAMNSMINTLCFVTYKNDTVKYFKKIMLLH 360  
 Db 301 YGFTIVRDFPPTVFKVKEHYLTAFAIVECIAMNSMINTLCFVTYKNDTVKYFKKIMLLH 360  
 QY 361 WKASYNG 367  
 Db 361 WKASYNG 367

RESULT 14  
 ABG94403  
 ID ABG94403 standard; Protein; 393 AA.  
 XX AC ABG94403;  
 XX DT 27-NOV-2002 (first entry)  
 XX DE Rat GPCR protein rZAQ1.  
 XX KW G-protein coupled receptor; GPCR; ZAQ; human; ZAQ; ZAQ; rat; ZAQ1;  
 KW rZAQ1; rZAQ2; mouse; I5E receptor; m15E; GPR73; Bv8 protein; M15;  
 KW digestive disorder; central nervous system disorder; CNS; diarrhoea;  
 KW bowel inflammation; constipation; food absorption disorder; nootropic;  
 KW Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;  
 KW antiinflammatory; antididiarrhoeic; neuroleptic; neuroprotective;  
 XX OS Rattus sp.  
 XX PN WO200262944-A2.  
 XX PD 15-AUG-2002.  
 XX PF 01-FEB-2002; 2002WO-JP00852.  
 XX PR 02-FEB-2001; 2001JP-0026820.  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;  
 PI Hinuma S;  
 DR WPI: 2002-627537/67.  
 DR N-PSDB; ABS71123.  
 XX Screening of compounds modifying the binding of G-protein coupled  
 PT receptor protein ZAQ and related proteins to their ligands for use in  
 PT treatment and diagnosis of digestive disorders .  
 XX Claim 1; Page 176-178; 197pp; Japanese.

The present invention relates to a screening method for compounds  
 for their ability to modify the binding of G-protein coupled receptor  
 (GPCR) protein ZAQ and related proteins (human ZAQ, human ZAQ1,  
 rat ZAQ1 (rZAQ1), rZAQ2, human and mouse I5E (m15E) receptor, and  
 mouse GPR73) to their ligands (the mature form of human, mouse or rat  
 Bv8 protein). The receptor protein and ligand are contacted in the  
 presence or absence of the test compound. The compounds are useful  
 in a drug composition for the treatment, and prevention of digestive  
 and central nervous system (CNS) disorders, including bowel  
 inflammation, diarrhoea, constipation, food absorption disorders,  
 Alzheimer's disease, Parkinson's disease and schizophrenia.  
 The present sequence represents a GPCR or related protein.

Sequence 393 AA;  
 Query Match 86.0%; Score 1767; DB 23; Length 393;

Best Local Similarity 84.0%; Pred. No. 4.8e-194;  
 Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTWGFMDDNATNTSFLSVLNPBGAAHATSPFNFSYSDYDMPLEDEEDVTSRITFFA 60  
 Db 1 METTVGLIGENTTNTFTDFFSARDGSGAETSPLEFTFSYGDYDMPSEDEEDVTSRITFFA 60  
 QY 61 AKIVIGMALVIGIMLVCGIGNEIFITAAIVRYKKRLNLLIANLAISDFLVAIVCCPFEM 120  
 Db 61 AKIVIGMALVIGIMLVCGIGNEIFITAAIVRYKKRLNLLIANLAISDFLVAIVCCPFEM 120  
 QY 121 DYYVVRQLSWEHGHVLCASVNLRTVSLVYSTNALLAIAIDRYLAIYVHPLRPMKQCOTAT 180  
 Db 121 DYYVVRQLSWEHGHVLCASVNLRTVSLVYSTNALLAIAIDRYLAIYVHPLRPMKQCOTAA 180  
 QY 181 GLIALVMTVSYLIIAIPSAFYTTTETVLIVIVKSOEIKFCGQWPDQOLYKYSFLFPIGIE 240  
 Db 181 GLIFLWMSVSLIIAIPSAFYTTTETVLIVIVKSOEIKFCGQWPDQOLYKYSFLFPIGIE 240  
 QY 241 FVGPPVMTLTCVARIISRELWFKAVPGFQEQIRKRLRCRKTVLVLMCLITAYVLCWAPF 300  
 Db 241 FVGPPVMTLTCVARIISRELWFKAVPGFQEQIRKRLRCRKTVLVLMCLITAYVLCWAPF 300  
 QY 301 YGFTIVRDFPPTVFKVKEHYLTAFAIVECIAMNSMINTLCFVTYKNDTVKYFKKIMLLH 360  
 Db 301 YGFTIVRDFPPTVFKVKEHYLTAFAIVECIAMNSMINTLCFVTYKNDTVKYFKKIMLLH 360  
 QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICRLK 393  
 Db 361 WRASPSGSKASADLDLRTTGIPATEEVDICRLK 393

RESULT 15  
 ABB99158  
 ID ABB99158 standard; Protein; 393 AA.  
 XX AC ABB99158;  
 XX DT 15-NOV-2002 (first entry)  
 XX DE Rat rZAQ1 protein.  
 XX KW Rat; physiological; G protein-coupled receptor; ZAQ; antididiarrheic;  
 KW laxative; anti-inflammatory; digestive disease; diarrhoea; constipation;  
 KW colitis; gene therapy; rZAQ1.  
 XX OS Rattus sp.  
 XX PN WO200262996-A1.  
 XX PD 15-AUG-2002.  
 XX PF 01-FEB-2002; 2002WO-JP00837.  
 XX PR 02-FEB-2001; 2001JP-0026798.  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX PI Ohtaki T, Masuda Y, Takatsu Y;  
 XX WPI: 2002-627554/67.  
 XX N-PSDB; ABQ79092.

Physiologically-active brain-originated G protein-coupled receptor  
 PT peptide ZAQ and encoding DNA, useful for developing drugs to treat  
 PT digestive diseases e.g. diarrhoea, constipation and colitis, including  
 PT gene therapy .  
 XX Claim 16; Page 161-163; 184pp; Japanese.

The invention relates to a novel physiologically-active brain-originated  
 CC G protein-coupled receptor peptide designated ZAQ. The proteins of the  
 CC invention have antididiarrheic, laxative, and anti-inflammatory activity.

CC The DNA and encoded protein are useful for developing drugs for the  
CC treatment of diseases of the digestive organs e.g. diarrhoea,  
CC constipation and colitis. The polynucleotides may have a use in gene  
CC therapy. The sequence represents a rat ZAG (rZAG1) protein of the  
CC invention.

XX

SQ Sequence 393 AA;

```
Query Match      86.0%; Score 1767; DB 23; Length 393;
Best Local Similarity 84.0%; Pred. No. 4.8e-194;
Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 METTMGFMDNATNTSTSLVNLPHGHATSPFPNFYSYSDYDMPDDEDEDTNSRTFFA 60
Db   |||| : : ||| : : : || : ||| |||| ||:|||||
QY 1 METTVGLGENTNTTDFSGADSGATSPLPFTFSYGYDMPDSEEDVTNSRTFFA 60
Db   |||| : : ||| : : : || : ||| |||| ||:|||||
QY 61 AKIVIGMALVGMVCGIGNFIPFIALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120
Db   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 61 AKIVIGMALVGMVCGIGNFIPFITALARYKKLRNLTNLLIANLAISDFLVAIVCCPFEM 120
Db   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 121 DXYVVRQLSWEHGHVLTQVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQAT 180
Db   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 121 DXYVVRQLSWEHGHVLTQVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQATA 180
Db   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 181 GLIALVTVSILIAIPSAFTTETVLVIVKSEKIFCGQIPVDQOQYKSYFLFIFGIE 240
Db   ||| |||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||
QY 181 GLIFLWVSILIAIPAAFTTETVLVIVESQEKIFCGQIPVDQOQFYRSYFLLVFGL 240
Db   ||| |||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||
QY 241 FVGPTVTHLTCYARISRELWFKAVPGFQTEQIRKRLRCRRKTVLVMCILTAYVLCWAPF 300
Db   |||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 241 FVGPIAMTLCYARVSRELWFKAVPGFQTEQIRRLRCRRRTVLGVCVLSAYVLCWAPF 300
Db   |||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 301 YGFTIVRDFPFTVYVKEKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
Db   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||
QY 301 YGFTIVRDFPSPVYVKEKHYLTAFYIVECIAMNSMINTLCFVTVVRNNTSKYLKRLRLQ 360
Db   |||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 361 WKASYNGKSSADLDLKTIGMPATEEVDCIRLK 393
Db   || : || : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 361 WRASPSGSKASADLDLRTTGIPATEEVDCIRLK 393
Db   || : || : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
```

Search completed: October 7, 2003, 09:51:48  
Job time : 46 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:49:27 ; Search time 19 Seconds  
(without alignments)  
1989.173 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTMGFMDNATNTSTSL.....LDLKTGMPTATEEVDICRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 405   | 19.7        | 449    | 2 A41738 | neuropeptide Y rec  |
| 2          | 387.5 | 18.9        | 381    | 2 I39187 | neuropeptide Y/pep  |
| 3          | 387.5 | 18.9        | 519    | 2 S17783 | tachykinin receptio |
| 4          | 367.5 | 17.9        | 370    | 1 I52315 | G protein-coupled   |
| 5          | 363   | 17.7        | 384    | 2 S20303 | neurokinin 2 recep  |
| 6          | 362.5 | 17.6        | 407    | 2 A34357 | neurokinin 1 recep  |
| 7          | 360.5 | 17.5        | 407    | 2 S20304 | neurokinin 1 recep  |
| 8          | 356.5 | 17.3        | 407    | 1 JQ1274 | neurokinin 1 recep  |
| 9          | 354.5 | 17.3        | 407    | 2 S23510 | neurokinin 1 recep  |
| 10         | 354   | 17.2        | 384    | 2 I57957 | neurokinin 2 recep  |
| 11         | 354   | 17.2        | 398    | 1 JQ1059 | neurokinin 2 recep  |
| 12         | 347   | 16.9        | 384    | 1 S00516 | neurokinin 2 recep  |
| 13         | 340   | 16.5        | 402    | 2 I56595 | neurokinin 2 recep  |
| 14         | 338   | 16.4        | 390    | 2 A36737 | neurokinin 2 recep  |
| 15         | 334.5 | 16.3        | 391    | 2 A41795 | somatostatin recep  |
| 16         | 334.5 | 16.3        | 391    | 2 C41795 | somatostatin recep  |
| 17         | 334.5 | 16.3        | 391    | 2 A39297 | somatostatin recep  |
| 18         | 328.5 | 16.2        | 465    | 1 JQ1517 | neurokinin 3 recep  |
| 19         | 328.5 | 16.0        | 384    | 2 A47249 | brain-specific som  |
| 20         | 327   | 15.9        | 504    | 2 A41783 | tachykinin recepto  |
| 21         | 325.5 | 15.8        | 384    | 2 JQ4629 | somatostatin recep  |
| 22         | 324.5 | 15.8        | 452    | 2 A34916 | neurokinin 3 recep  |
| 23         | 321.5 | 15.6        | 349    | 2 I59336 | galanin receptor 1  |
| 24         | 320   | 15.6        | 375    | 2 S63685 | neuropeptide Y rec  |
| 25         | 320   | 15.6        | 385    | 2 S55524 | neurokinin 3 recep  |
| 26         | 319   | 15.5        | 440    | 2 A44081 | kappa-type opioid   |
| 27         | 314   | 15.3        | 357    | 2 JQ7319 | probable allatosta  |
| 28         | 309.5 | 15.1        | 423    | 2 B40470 | glucocorticoid-ind  |
| 29         | 309   | 15.0        | 394    | 2 JQ7209 | galanin receptor -  |

#### ALIGNMENTS

##### RESULT 1

A41738

neuropeptide Y receptor - fruit fly (Drosophila melanogaster)

N:Alternate names: G protein-coupled receptor PR4

C:Species: Drosophila melanogaster

C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 20-Apr-2000

C:Accession: A41738

R:Li, X.-J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992

A:Title: Cloning, functional expression, and developmental regulation of a neuropep

A:Reference number: A41738; MUID:92112730; PMID:1370455

A:Accession: A41738

A:Molecule type: mRNA

A:Residues: 1-449 <LIA>

A:Cross-references: GB:M81490; NID:gl57996; PIDN:AAA28727.1; PID:gl57997

C:Genetics:

A:Gene: FlyBase:Nepyr

A:Cross-references: FlyBase:FBgn0004842

C:Superfamily: neurokinin 1 receptor

C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

|                       |        |   |          |            |        |        |     |      |     |
|-----------------------|--------|---|----------|------------|--------|--------|-----|------|-----|
| Query Match           | 19.78; | Score   | 405;     | DB 2;      | Length | 449;   |     |      |     |
| Best Local Similarity | 30.0%; | Pred. No.   | 4.3e-27; |            |        |        |     |      |     |
| Matches               | 115;   | Conservative  | 70;      | Mismatches | 128;   | Indels | 70; | Gaps | 15; |
| Qy                    | 9      | DDNATN---TSTFSLVNLPHGAAHATFPNFYSYSDYDMLDEDEVDVNSRTFFAAKIVI    | 65       |            |        |        |     |      |     |
| Db                    | 41     | DBEGSNYGYGSTTSLGLOFETYNITVM--NMFSCDDYDL---LSEDMWSSAYF---KIIIV | 93       |            |        |        |     |      |     |
| Qy                    | 66     | GMALVGLMVCVGIGNFTFIAALVRYKKRLNLTNLLIANLAISDFLVAIVCCP-----FE   | 119      |            |        |        |     |      |     |
| Db                    | 94     | YMLYPIFIFALGTNGTVCYIVTSTPRMRTVNFYFIASLALGILMSFFCEPSSFSISLFI   | 153      |            |        |        |     |      |     |
| Qy                    | 120    | MDYVVVROLSEHGHHVLCVTSVNTLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKQTA    | 179      |            |        |        |     |      |     |
| Db                    | 154    | LNY-----WPGFALCHFEVNTSQAVSLVSAVTLVAISIDRYIALMPLKPRIKRYA       | 206      |            |        |        |     |      |     |
| Qy                    | 180    | TGLIALVWTVSILIAIP-----SAFTTETVLVIVKQSEKIFCCQIWPVDOOLY         | 228      |            |        |        |     |      |     |
| Db                    | 207    | TFIAGVMFIALATALPIVPIVGLDIPMSPHWT-----KCEYICREMPSPRSQEY        | 257      |            |        |        |     |      |     |
| Qy                    | 229    | YKSVFLFIFGIEFGVPVWTLCAVARSRLWFKAVPG-FOTEQIRKRLCRKRTVLVLAM     | 287      |            |        |        |     |      |     |
| Db                    | 258    | Y--YTSLFALQFVPLGVGLIFTYARITIRWAKRPGEAETNRDQMAKSKRWVQML        | 315      |            |        |        |     |      |     |
| Qy                    | 288    | CILTAYVLCNAPYFGFTVRD-----FFPTVFVKKHYLTAFYIVECIANSMSINTL-      | 340      |            |        |        |     |      |     |
| Db                    | 316    | TVIVFTCCWLPFNILQLLNDDEFAHMDPLPYV-----WFAFWLANSCHCCYNPII       | 367      |            |        |        |     |      |     |
| Qy                    | 341    | -CFYVVKNDVYKFKK--IMLLH  | 360      |            |        |        |     |      |     |
| Db                    | 368    | YCYMNAR-----FRSGFVQLMH  | 384      |            |        |        |     |      |     |

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DB      270 LVCVVVYFANSWLPLHAFQALVDISGV-LDLKEYKLIITVFHIAMCTSFANPLLIGHW 328
QY      346 KNDTVKYF 353
       :: | |
DB      329 NSNYRKAF 336

RESULT 3
SI7783
A:Title: tachykinin receptor homolog DTKR - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Apr-2000
C:Accession: SI7783
R.Lia, X.J.; Wolfqiang, W.; Wu, Y.N.; North, R.A.; Forte, M.
EMBO J. 10, 3221-3229, 1991
A:Title: Cloning, heterologous expression and developmental regulation of a Drosophila
A:Reference number: SI7783; MOID:92007772; PMID:1717263
A:Accession: SI7783
A:Molecule type: mRNA
A:Residues: 1-519 <Li>
A:Cross-references: EMBL:X62711; NID:g8505; PIDN:CAA44595.1; PID:g8506
A>Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in lacking 48
       C:Genetics:
A:Gene: FlyBase:Takr99D
A:Cross-references: FlyBase:FBgn0004622
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; neurotransmitter receptor; transmembrane pro-
Query Match          18.9%; Score 387.5; DB 2; Length 519;
Best Local Similarity 27.2%; Pred. No. 1.6e-25;
Matches 113; Conservative 82; Mismatches 148; Indels 73; Gaps 18;

QY      1 METTGFMD-----NATNTST-----SFLSVLN--PHGAHAITSPPF---NF 37
DB      1 MENRSDFEADDYGDISWSNWSNWSTPAGVLFSASMSVLSASNHTPCRTLARSSPYPPVSF 60
               ||| ||||| :||| | ||| | | | | | | | | | | | | | | | | |
QY      38 SYS----DYDNEL-----DEDEDV-----TSNRTEFA---AKIVIGMALVGIMLVCGIGNF 81
DB      61 NHSOTLSDDPAVGVEDAAEDAAASMETGSFAFVPWNROVLWSILFGOMVIATGGNL 120
               ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      82 IPTAALVKRYKLRLNTLLIANLAISOFLVAIVCCPEMDEVYVVRQLSWRHGHVLTCSVN 141
DB      121 IVVNIWMTRKTMTVTNVFYINLSADAWSSLNVTFF--NYIYMDSDFWFGEFYCKLSQ 178
QY      142 YLRTVSLXVSTNNALLAIADRYLAIVHPRLPRMKQCQTGLIALVWTVISIIAIPSAFT 201
DB      179 FIAMSICASFETTLMAISIDRYAVAIRLPDRPKRCRNLAIAAYWIWLASTLISCP----- 233
QY      202 TETVLIVIKYSQE-----KIFGGOIW---PVDOQLYKSYFLFEIGIEFGVPVVTML 250
DB      234 ---MMILIYTEEPYRGISNRTCVCPEPDGTNHSTMESLYNLIILLIIFYPIVSMTV 290
QY      251 CYARISRELWKAVPGFOTEIRKKHLRRKRVTLVMCLILTAYYLWCAPYGYFTIVRDFF 310
DB      291 TYSRVGIELWGSKTGICTPTPOVENVRSKRVAKNMIWVLLIFAICWLPFHSHFIITSCY 350
QY      311 PTV----FYKEKHYYLATVIVECIASSMNMTLCFTVTKNDTVKY-FKKIMLLHW 361
DB      351 PAITEAPPFIQEL-YLIAIW-----LANSMNTNPDIYCWH-NSRPRIYGF-K-MVFRW 398

RESULT 4
IS2315
G protein-coupled receptor UHR-1 - rat
C:Species: Rattus sp. [rat]
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C:Accession: IS2315
R.Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A:Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned f
A:Reference number: IS2315; MOID:95251659; PMID:7733930
A:Accession: IS2315
A>Status: preliminary; translated from GB/EMBL/DDBBJ

```

| Query Match           | 17.74; | Score 363;   | DB 2; | Length 384;                        |
|-----------------------|--------|--|-------|------------------------------------|
| Best Local Similarity | 27.08; | Pred. No. 1.5e-23;   |       |                                    |
| Matches               | 93;    | Conservative   | 69;   | Mismatches 136; Indels 46; Gaps 9; |
| Qy                    | 8      | MDONATWTSFSLVLPNGAHATSFPEFNFYSYDMPFLDEDEDEVTNSRTFAAKIVGM     | 67    |                                    |
| Db                    | 1      | MGAHVSVDINILSGIESNATGVTA-----FSMPGWQLAL-----                 | 38    | WAT                                |
| Qy                    | 68     | ALVGMILVCGIGNFIFTAALVRYKKKLNLLNLANLAISDFLVAIVCCPEMDYVVVRQ    | 127   |                                    |
| Db                    | 39     | AYTALVLVAVTGNATVITWIIIAHERMTVTNYFTINLALADLCAAFNATFNFIY--ASH  | 96    |                                    |
| Qy                    | 128    | LSWEGHGVLCITSVYKLRVTSVYSYFNALLATAIDRYLAIVHPLPRMKQCATGLIALVW  | 187   |                                    |
| Db                    | 97     | NIWTFGSTFCYFQNLFPVTAMFVSLYKSTALAADRYMAIVHPQRLSAPSTKAVIAVW    | 156   |                                    |
| Qy                    | 188    | TVSILIIAIPSAFTTETVLVIVKSOEKIFCGQIWPVQ-----OLYYKSYFLFIQIEFV   | 242   |                                    |
| Db                    | 157    | LVALALASPOCFYGTITV-----DQGATKCVVAVPNDNGGKMLLLYHLVWPLVIFL---- | 208   |                                    |





Db 234 DRYHEQVSAKRKVKVMHVVVCTFAICWLPFHIFLLPYINPDLYLK-KFIQQVYLAIMW 292  
QY 330 IAMSNSMINTLCFTVYKND 348  
Db 293 LAMSSTWNPNIYCCCL-ND 310

RESULT 9  
S23510  
neurokinin 1 receptor - guinea pig  
N:Alternate names: NK-1 receptor; substance P receptor  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 19-May-2000  
C:Accession: S23510; S19198  
R:Gorbulev, V.; Akhundova, A.; Luzius, H.; Fahrenholz, F.  
Biochim. Biophys. Acta 1131, 99-102, 1992  
A:Title: Molecular cloning of substance P receptor cDNA from guinea-pig uterus.  
A:Reference number: S23510; MUID:92256498; PMID:1374648  
A:Accession: S23510  
A:Molecule type: mRNA  
A:Residues: 1-407 <GOR>  
A:Cross-references: EMBL:X64323; NID:949565; PIDN:CAA45608.1; PID:949566  
C:Superfamily: neurokinin 1 receptor  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:32-55/Domain: transmembrane #status predicted <TM1>  
F:69-89/Domain: transmembrane #status predicted <TM2>  
F:117-128/Domain: transmembrane #status predicted <TM3>  
F:149-169/Domain: transmembrane #status predicted <TM4>  
F:196-217/Domain: transmembrane #status predicted <TM5>  
F:250-280/Domain: transmembrane #status predicted <TM6>  
F:289-308/Domain: transmembrane #status predicted <TM7>

Query Match 17.3%; Score 354.5; DB 2; Length 407;  
Best Local Similarity 24.8%; Pred. No. 8.5e-23;  
Matches 79; Conservative 85; Mismatches 134; Indels 21; Gaps 9;

QY 41 DYDMLPDED-----EDVTSRTFF--AAKIVIGMALVGLMVLGCG-IGNFIFTAALVRYK 91  
Db 2 DNVLPVSDLPFNISTNTSEPNQVQPAQWQVLAIAATVITVTSVGVNVMVMIILAHK 61

QY 92 KLRNLTLNLTANLAISDFVAIVCCPEMDYVYVYRQLSWEGHVLCSTVNYLRYSLVYS 151  
Db 62 RMRVTVTYFLVNLAFABASMAAFTVNVFTYAVHNE--WYGLFYCKFHFPFPAAFAS 119

QY 152 TNALLATAIDRYLAIVHPLRPMKQATGLIALVWTVTSILAIAPSAVF-TTEVLVIVK 210  
Db 120 IYSTAVAFDRYMAIIHPLQRLSATATKVCVCIWVLAULLAFPGGYSTETM----- 174

QY 211 SQEKFQCIQWVY-DOQLYKYSYFLFIFGIEFVGVPVMTLCYARISRELWFKAVPGFOT 269  
Db 175 -PGRVVCMIENPSHPDKIYERKVIYHICVTLVLYFLPLVIGVAYTVWGTLLWASEIPGDS 233

QY 270 EQIRKRLRCRKTVLVLMCILTAVLWCAPIYGFIVRDFPPTVFKKHYLTAFYIVEC 329  
Db 234 DRYHEQVSAKRKVKVMHVVVCTFAICWLPFHIFLLPYINPDLYLK-KFTQQVYLAIMW 292

QY 330 IAMSNSMINTLCFTVYKND 348  
Db 293 LAMSSTWNPNIYCCCL-ND 310

RESULT 10  
I57957  
neurokinin 2 receptor - hamster  
N:Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)  
C:Species: Cricetinae gen. sp. (hamster)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
C:Accession: I57957  
R:Aharony, D.; Little, J.; Thomas, C.; Powell, S.; Berry, D.; Graham, A.  
Mol. Pharmacol. 45, 9-19, 1994  
A:Title: Isolation and pharmacological characterization of a hamster urinary bladder neu  
A:Reference number: I57957; MUID:94134065; PMID:8302285  
A:Accession: I57957

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-384 <RES>  
A:Cross-references: GB:S68899; NID:9545230; PIDN:AAC60680.1; PID:9545231  
C:Superfamily: neurokinin 1 receptor

Query Match 17.2%; Score 354; DB 2; Length 384;  
Best Local Similarity 27.4%; Pred. No. 8.8e-23;  
Matches 94; Conservative 65; Mismatches 140; Indels 44; Gaps 10;

QY 8 MDNATNTSTSLSVLNPNGAHATSPFFNFSTSDYDMPLEDEDTNSTRFFAAKIVI-G 66  
Db 1 MCGRAIVTDTNIFSGLESNTGTAF-----SMP-----AWQLALWA 37

QY 67 MALVGLMVLGCGIGNFFIAALVYKRLNLTLLIANLAISDFVAIVCCPEMDYVYVVR 126  
Db 38 TAYLGLVAVTGNATVIMIIIAHERRTVYWFINLALADLCMAFNATNFVY--AS 95

QY 127 QLSWEGHVLCSTVNYLRTVSLVSTNALLATIDRYLAIVHPLRPMKQATATGLIALY 186  
Db 96 HNIWYFGRAFCYFQNLFPITAMFVSIYSTAIAADRYMAIVHVPQRLSAPITKATIAGI 155

QY 187 WTVSILAIAPSAVFTTETVLVIVKSEKIFCGQIWPYD---QQLYKYSYFLFIFGIEFVG 243  
Db 156 WLVALALASQCCFYSTIV-----DQCATKCVVAMPNDNGKMLLL--YHLVVVFLVYFL 208

QY 244 PVTMTLCYARISRELWFKAVPGFQTEIRKR-LRCRRKTVLVMCILTAIVLWCAPIYGF 302  
Db 209 PLVYMFVAVSIGLTWKRVPYRHOAGNLRHLHAKKFKYKAVLVLTFAICWLPYHL 268

QY 303 FTIVRDFPPTVYVK---EKHYLPAFYIVECIAMNSMINTLCF 342  
Db 269 YFILGSGFKDIYVRKFTQQVYLTALFW----LAMSSTWNPNIY 307

RESULT 11  
JQ1059  
neurokinin 2 receptor - human  
N:Alternate names: neurokinin A receptor; NK-2 receptor; substance K receptor (SKR)  
C:Species: Homo sapiens (man)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JQ1059; JS0575; A23658; A61224  
R:Graham, A.; Hopkins, B.; Powell, S.J.; Danks, P.; Briggs, I.  
Biochem. Biophys. Res. Commun. 177, 8-16, 1991  
A:Title: Isolation and characterization of the human lung NK-2 receptor gene using  
A:Reference number: JQ1059; MUID:91254341; PMID:1710456  
A:Accession: JQ1059  
A:Molecule type: DNA  
A:Residues: 1-398 <GRA1>  
A:Cross-references: GB:M75105; NID:9189219; PIDN:AAB05897.1; PID:g189222  
A:Accession: JS0575  
A:Molecule type: mRNA  
A:Residues: 1-398 <GRA2>  
A:Cross-references: GB:M75105; NID:9189219; PIDN:AAB05897.1; PID:g189222  
A:Experimental source: lung  
A>Note: 23-Ile and 375 His were also found  
R:Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.  
J. Biol. Chem. 265, 20455-20462, 1990  
A:Title: The human neurokinin A (substance K) receptor. Molecular cloning of the ge  
A:Reference number: A23658; MUID:91056095; PMID:2173708  
A:Accession: A23658  
A:Molecule type: DNA  
A:Residues: 1-22, 'I', 24-240, 'L', 242-398 <GER>  
A:Cross-references: GB:M60284; GB:J05680; NID:g189140  
A>Note: the authors translated the codon GGA for residue 317 as Glu  
R:Kris, R.M.; South, V.; Saltzman, A.; Felder, S.; Ricca, G.A.; Jaye, M.; Huebner, I  
Cell Growth Differ. 2, 15-22, 1991  
A:Title: Cloning and expression of the human substance K receptor and analysis of i  
A:Reference number: A61224; MUID:91175483; PMID:1848773  
A:Accession: A61224  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-22, 'I', 24-293, 'F', 294-374, 'H', 376-398 <KRI>





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:47:46 ; Search time 15 seconds  
(without alignments)  
1232.100 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 METTMGFMDDNATNTSTSL.....LDLTIGMPATEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | ID            | Description         |
|------------|-------|---------------|--------|---------------|---------------------|
| 1          | 416.5 | 20.3          | 385    | 1 NY2R_CHICK  | Q9ddn6 gallus gall  |
| 2          | 405   | 19.7          | 449    | 1 NYR_DRONE   | P25931 drosophila   |
| 3          | 393.5 | 19.1          | 382    | 1 NY2R_PIG    | O02836 mus scrofa   |
| 4          | 391   | 19.0          | 384    | 1 NY2R_BOVIN  | P79113 bos taurus   |
| 5          | 390.5 | 19.0          | 385    | 1 NY2R_MOUSE  | P97295 mus musculus |
| 6          | 387.5 | 18.9          | 381    | 1 NY2R_HUMAN  | P49146 homo sapien  |
| 7          | 387.5 | 18.9          | 519    | 1 TLR2_DRONE  | P30975 drosophila   |
| 8          | 384.5 | 18.7          | 381    | 1 NY2R_MACAU  | Q9gk74 macaca mula  |
| 9          | 379   | 18.4          | 381    | 1 NY2R_CAYPO  | Q9z2d5 cavia porce  |
| 10         | 370   | 18.0          | 370    | 1 GP10_HUMAN  | P49683 homo sapien  |
| 11         | 367.5 | 17.9          | 370    | 1 GP10_RAT    | Q64121 rattus norv  |
| 12         | 363   | 17.7          | 384    | 1 NK2R_MOUSE  | P30549 mus musculus |
| 13         | 362.5 | 17.6          | 407    | 1 NK1R_RAT    | P14600 rattus norv  |
| 14         | 360.5 | 17.5          | 407    | 1 NK1R_MOUSE  | P30548 mus musculus |
| 15         | 358   | 17.4          | 384    | 1 NK2R_RABIT  | P79218 oryctolagus  |
| 16         | 356.5 | 17.3          | 407    | 1 NK1R_HUMAN  | P25103 homo sapien  |
| 17         | 354.5 | 17.3          | 407    | 1 NK1R_CAYPO  | P30547 cavia porce  |
| 18         | 354   | 17.2          | 384    | 1 NK2R_MESCAT | P51144 mesocricetu  |
| 19         | 354   | 17.2          | 398    | 1 NK2R_HUMAN  | P21452 homo sapien  |
| 20         | 351   | 17.1          | 425    | 1 OX1R_MOUSE  | O43613 homo sapien  |
| 21         | 347   | 16.9          | 384    | 1 NK2R_BOVIN  | P05363 bos taurus   |
| 22         | 347   | 16.9          | 416    | 1 OX1R_RAT    | P36718 rattus norv  |
| 23         | 345   | 16.8          | 444    | 1 OX2R_HUMAN  | O43614 homo sapien  |
| 24         | 344   | 16.7          | 460    | 1 OX2R_MOUSE  | P58308 mus musculus |
| 25         | 343.5 | 16.7          | 444    | 1 OX2R_CANFA  | Q8tup7 canis fami   |
| 26         | 343   | 16.7          | 460    | 1 OX2R_RAT    | P36719 rattus norv  |
| 27         | 340   | 16.5          | 402    | 1 NK2R_CAYPO  | Q64077 cavia porce  |
| 28         | 339.5 | 16.5          | 408    | 1 NK1R_RANCA  | Q98982 rana catesb  |
| 29         | 338   | 16.4          | 390    | 1 NK2R_RAT    | P16610 rattus norv  |
| 30         | 337   | 16.4          | 346    | 1 GALR_RAT    | Q62805 rattus norv  |
| 31         | 336   | 16.4          | 348    | 1 GALR_MOUSE  | P36479 mus musculus |
| 32         | 335   | 16.3          | 422    | 1 GP72_CANFA  | Q9ttq9 canis fami   |
| 33         | 335   | 16.3          | 504    | 1 TLR1_DRONE  | P30974 drosophila   |

RESULT 1  
NY2R\_CHICK  
ID NY2R\_CHICK STANDARD; PRT; 385 AA.  
AC Q9DDN6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).  
GN NPY2R.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OC NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20532533; PubMed=11078884;  
RA Salanek E., Holmberg S.K., Berglund M.M., Boswell T., Larhammar D.;  
RT Chicken neuropeptide Y receptor Y2: structural and pharmacological  
RT differences to mammalian Y2.\*;  
RL FEBS Lett. 484:229-234(2000).  
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC HIGHEST TO TACHYKININS RECEPTORS.

#### ALIGNMENTS

|    |       |      |     |   |            |                     |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 334.5 | 16.3 | 391 | 1 | SSR1_HUMAN | P30872 homo sapien  |
| 35 | 334.5 | 16.3 | 391 | 1 | SSR1_MOUSE | P30873 mus musculus |
| 36 | 334.5 | 16.3 | 391 | 1 | SSR1_RAT   | P28646 rattus norv  |
| 37 | 332.5 | 16.2 | 465 | 1 | NK3R_HUMAN | P29371 homo sapien  |
| 38 | 328.5 | 16.0 | 384 | 1 | SSR4_RAT   | P30937 rattus norv  |
| 39 | 327.5 | 15.9 | 467 | 1 | NK3R_RABIT | O97512 oryctolagus  |
| 40 | 327   | 15.9 | 371 | 1 | NY6R_MOUSE | Q61212 mus musculus |
| 41 | 327   | 15.9 | 452 | 1 | NK3R_MOUSE | P47937 mus musculus |
| 42 | 325.5 | 15.8 | 384 | 1 | SSR4_MOUSE | P49660 mus musculus |
| 43 | 325.5 | 15.8 | 423 | 1 | GP72_HUMAN | O9nym4 homo sapien  |
| 44 | 324.5 | 15.8 | 452 | 1 | NK3R_RAT   | P16177 rattus norv  |
| 45 | 321.5 | 15.6 | 349 | 1 | GALR_HUMAN | P47211 homo sapien  |

```

FT DOMAIN 333 385 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 127 207 BY SIMILARITY.
FT LIPID 346 346 PALMITATE (POTENTIAL).
SQ SEQUENCE 385 AA; 43509 MW; 60A09B314E665B62 CRC64;

Query Match
Best Local Similarity 30.3%; Score 416.5; DB 1; Length 385;
Matches 93; Conservative 75; Mismatches 132; Indels 7; Gaps 4;

QY 43 DMPLDEDEVTNSRTFFRAKIVIGMALVIMVCGIGNFIFIAALVRYKKRLNLTLLIA 102
DB 35 ELALDPKPKLSTLVEVOIILIPAYGSIILLVIGNSLVHVIKPKSMRTVTFNFFIA 94
QY 103 NLAISDFVAIVCCPFEMDYVVRQSLSEHGHLVCTSVNLTSTVSLVSTNALLAIDR 162
DB 95 NLAVALDLVNTLCLEFTLVYLLGE--NKLGPVLCHLVYQAALAVHVTVTLVIALDR 152
QY 163 YLAIVHLPRLMKCOTATGLIALVMTSILIAIPSAFTTETVLVIVKSEKIFCGIWP 222
DB 153 HRCIVVHLESKISKISFLIGVAVASALLASPLAFREYSLEIIPDFKIVVCSKWP 212
QY 223 VDQQLYYAS-YELFTFEGIEFVCPVVTMTLCYARISRELWFKAVPGFQTEQKRLCRK 281
DB 213 GEGQNYGTIYSVSMLLIQVLPALISYATRIWTKLNHVSPOGANDHYHHR---RQK 269
QY 282 TVLVLMCLITAVLVCAWPFYGTIVRDFPTVFVKEKHYLTAFYIVECIAMNSMINTLC 341
DB 270 TTKMLVCVVVFAVSWLPHAFQLVSDSDSQV-LDLKEYKLIYTVFHVIMCSFANPLL 328
QY 342 FVTYVND 348
DB 329 YGWMANN 335

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RESULT 2
NYR_DROME STANDARD; PRT; 449 AA.
AC P25931;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Neuropeptide Y receptor (NPY-R) (NP4 receptor).
GN NEPYR.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112730; PubMed=1370455;
RA Li X.-J., Wu Y.-N., North R.A., Forte M.;
RT *Cloning, functional expression, and developmental regulation of a
RT neuropeptide Y receptor from Drosophila melanogaster.;
RL J. Biol. Chem. 267:9-12(1992).
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DEVELOPMENTAL STAGE: AT LOW LEVELS DURING EARLY EMBRYONIC STAGES,
CC ITS EXPRESSION INCREASES LATER AND REACHES THE HIGHEST LEVEL
CC DURING LATE STAGES OF EMBRYOGENESIS. SUBSEQUENTLY, PRA LEVELS ARE
CC REDUCED DURING LARVAL STAGES AND INCREASE DURING PUPAL STAGES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
CC -----
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CC -----

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DR EMBL; M81490; AAA28727.1; -.
DR PIR; A41738; A41738.
DR Flybase; FBgn004842; Npyr.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPS.
DR PROSITE; PS00237; G-PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 85 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 86 111 1 (POTENTIAL).
FT DOMAIN 112 120 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 121 145 2 (POTENTIAL).
FT DOMAIN 146 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 187 3 (POTENTIAL).
FT DOMAIN 188 203 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 204 232 4 (POTENTIAL).
FT DOMAIN 233 256 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 282 5 (POTENTIAL).
FT DOMAIN 283 309 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 310 330 6 (POTENTIAL).
FT DOMAIN 331 347 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 348 372 7 (POTENTIAL).
FT DOMAIN 373 449 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 449 AA; 51885 MW; IADB32EPD50146C3 CRC64;

Query Match 19.7%; Score 405; DB 1; Length 449;
Best Local Similarity 30.0%; Pred. No. 8.7e-22;
Matches 115; Conservative 70; Mismatches 128; Indels 70; Gaps 15;

QY 9 DDNATN---TSTSLSVLPHGAHATSPFNFSYSDYDMLDDEDEVTNSRTFAAKIVI 65
DB 41 DDEGSNYGSGTTLTSLGLQFETYNITVM-MNFCDDYDL---LSEDMWSAYF---KIIY 93
QY 66 GMALVGLMVGCGIGNFIFIAALVRYKKRLNLTLLIAISDFLVAIVCCP-----FE 119
DB 94 YMLYIPFIPALIGNTCVYIVSTPRMRTVNYFIASLDILMGFFCEPSSFSISLFI 153
QY 120 MDYVYVQLSWEHGHVLTSTVNYLRTVSLYSTVALLAIAIDRYLAIVHLPRLMKCQTA 179
DB 154 LNY-----WPGFALCHFYNSQAVSVLVSYTVAISIDRYIAIMWPLKPRITRYA 206
QY 180 TGLIALVMTVSILTAIP-----SAFTTETVLVIVKSEKIFCGIWPVDQQLY 228
DB 207 TFIAGVWFIALATALPIPIVSGLDIPMSPHRT-----KCEKYICREMWPSRQSEY 257
QY 229 YKSYELFIFIGIEFVGVVMTPLCYARISRELWFKAVPG-FQTEQKRLCRKRTVLVLM 287
DB 258 Y--YTLSLFALQFVPLGLVLTFTYARITIRWAKRPPGEAETNRDQRMARSKRMVKML 315
QY 288 CILRAYVLCAWPFYGTIVRD-----FFPVPVFKKHYLTAFYIVECIAMNSMINTL- 340
DB 316 TVVITVCCMLPFLNQLLLNDEEFAHWDPLPYV-----WFAFWLWAMSHCCYPII 367
QY 341 -CFVTYVNDTVKYPK--IMLLH 360
DB 368 YCYNNAR-----FRSGFVQLMH 384

RESULT 3
NY2R_PIG STANDARD; PRT; 382 AA.
AC O02836; O2ST11;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-v2 receptor).
GN NP2R.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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47 DEDEDVTSNRTEFAAKIVIGMALVGVIMLVCGIGNFIFIAALVRYKRLRLNLTNLLIANLAI 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
36 DSEPELAKDSTKLIEQIILILAYCSIIILGVVGNLSIVHWIKFKSMRTVTNFFIANLAV 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
107 SDFELAVCCCPPEMDYVYVVRQIISWEHGHVLCISVNYLRTVSLVYSTNALLAIDAIDRYLAI 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
96 ADLLVNTLCLPFTLTATLGE--WKMGPPVLCILPYPAOGLAVQVSTITLTIVIALDRHRCI 153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
167 VHLPRMKCQATGILIALVMTVSIILAIIPSAVFTTETVLIVIVKSOEKFICGOIWPVDQ 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
154 VTHLESKISKRISFLIGLWAGISALASPLAIFREYSLEIIPDEIVACTEKWPEEK 213
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227 -LYYKSYFLFIRGIEFVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
214 SIYGTVYSLSSLLILVPLGIISFYARIWSKLNHVSPGGVNDYHQR---RQATTKM 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
286 LMCILTAYVLCHAPYGFYIVRDFPTFYVKEKHLYTARYIVECIAMSSMINTLCFVTV 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
271 LVCVVVFAVSLPLHAFQLAVIDSQV-LDLKEYKLIFTVFIHIIAMCSFTANPLLYGWM 329
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
346 KNDTVKIF-----KKIMLHWKASYNGKSSADLDLKTIGMP 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
330 NSNYRKAFLSAFCEQRIDAIHSEVSWT-SKAKKNLEATNGGP 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
NY2R_BOVIN
AC NY2R_BOVIN STANDARD; PRT; 384 AA.
ID P79113.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY_Y2 receptor).
GN NPY2R.
GE Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Annan D.A., Kolakowski L.F. Jr., Eadie D.M., Wong D.J., Ma Y.Y.,
RR Yang-Feng T.L., Thompson D.A.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YV.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U50144; AAB40600.1; -.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSN.
CC PROSITE: PS00237; G_PROTEIN_RECEP_FL1; 1.
CC PROSITE: PS50262; G_PROTEIN_RECEP_FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 53 75 1 (POTENTIAL).
CC DOMAIN 76 85 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 86 107 2 (POTENTIAL).
CC DOMAIN 108 127 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 128 149 3 (POTENTIAL).
CC DOMAIN 150 169 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 170 190 4 (POTENTIAL).

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|                          |       |                    |            |             |
|--------------------------|-------|--------------------|------------|-------------|
| Query Match              | 19.1% | Score 393.5;       | DB 1;      | Length 382; |
| Best Local Similarity    | 28.2% | Pred. No. 4.9e-21; |            |             |
| Matches 97: Conservative | 82;   | Mismatches 150;    | Indels 15; | Gaps 6;     |

FT DOMAIN 191 217 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 218 243 5 (POTENTIAL).  
 FT DOMAIN 244 271 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 272 294 6 (POTENTIAL).  
 FT DOMAIN 295 307 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 308 331 7 (POTENTIAL).  
 FT DOMAIN 332 384 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 126 206 BY SIMILARITY.  
 FT LIPID 345 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 384 AA; 42943 MW; 468D19CBA8F29681 CRC64;  
  
 Query Match 19.0%; Score 391; DB 1; Length 384;  
 Best Local Similarity 28.6%; Pred. No. 7.4e-21;  
 Matches 100; Conservative 77; Mismatches 159; Indels 14; Gaps 5;  
  
 QY 5 MGFMDNATNTSTFLSVLNPHGAHATSPFNFSVDYDMPDEDEDTNSRTFAKIV 64  
 DB 3 MGLPAGAEADENQTVEMKVDQFGPGHHTLP-----GELAPDSEPELIDSTKLEIYQV 55  
 QY 65 IGMALVGLMVGIGNFIIFIAALVRYKRLNLTLLIANLAISDFLVAIVCCPFEMDYV 124  
 DB 56 LILAYCSIIILGVIGNSLVHVIKFSKRTVTNFFIANLAVADLLVNTLCGLPFTLYTL 115  
 QY 125 VROLSEHGHLVCTSVNLTSTVSLVSNALLAIAIDRYLAIVHPLRPMKQATGLIA 184  
 DB 116 MGE--WKMGVPLCHLVPAQGLAVQVSTITLTVALDRHRCIVYHLESKISKQISFLIG 173  
 QY 185 LVMTYSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDOQ-LYIKSYELFIFGIEFVG 243  
 DB 174 LAMGVSAALLASPLAIFREYSLEIIPDFEIVACTEKWPEEGEKGITYSLSLLILYVL 233  
 QY 244 PVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRRTKTLVLMCILTAIVYLCWAPFYGF 303  
 DB 234 PLGIISFSYTRISKLKHNHVSQAHDYHQR---RQKTKMLVCVVVVEAVSNLPLHAF 290  
 QY 304 TIVRDEFTTVFVKEKHYLTAFYIVECIAMSNMINTLCFVTVKNDTVKYF 353  
 DB 291 QLAVIDSHV-LDLKEYKLIETVFHIIAMCSTFANPLLYGWNNSYKRAF 339  
  
 RESULT 5  
 NY2R\_MOUSE  
 ID NY2R\_MOUSE STANDARD; PRT; 385 AA.  
 AC P97295;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).  
 GN NPY2R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97071731; PubMed=8914576;  
 RA Nakamura M., Aoki Y., Hirano D.;  
 RT "Cloning and functional expression of a cDNA encoding a mouse type 2  
 RT neuropeptide Y receptor";  
 RL Biochim. Biophys. Acta 1284:134-137(1996).  
 CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO TACHYKININS RECEPTORS.  
 CC -----  
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 CC EMBL; D86238; BAA13050.1; --  
 CR MGD; MG1108418; NPY2R.  
 DR GO: GO:0001601; F:Peptide YY receptor activity; IDA.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEPT\_FL\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 54 76 1 (POTENTIAL).  
 FT DOMAIN 77 86 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 87 108 2 (POTENTIAL).  
 FT DOMAIN 109 128 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 129 150 3 (POTENTIAL).  
 FT DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 171 191 4 (POTENTIAL).  
 FT DOMAIN 192 218 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 219 244 5 (POTENTIAL).  
 FT DOMAIN 245 272 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 273 295 6 (POTENTIAL).  
 FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 309 332 7 (POTENTIAL).  
 FT DOMAIN 333 385 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 127 207 BY SIMILARITY.  
 FT LIPID 346 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 385 AA; 5AD7E4C9B7077085 CRC64;  
  
 Query Match 19.0%; Score 390.5; DB 1; Length 385;  
 Best Local Similarity 26.9%; Pred. No. 8e-21;  
 Matches 104; Conservative 89; Mismatches 168; Indels 25; Gaps 9;  
  
 QY 1 MEITMGFMDNATNTSTFLSVLNPHG-AHATSPFNFSVDYDMPDEDEDTNSRTFF 59  
 DB 1 MVLKMGVPGAEADENQTVEMKV-EPYGPHTT-----PRGELPPDPELIDSTKLV 51  
 QY 60 AAKIVGMALVGLMVGIGNFIIFIAALVRYKRLNLTLLIANLAISDFLVAIVCCPFE 119  
 DB 52 EVQVILILAYCSIIILGVIGNSLVHVIKFSKRTVTNFFIANLAVADLLVNTLCGLPFT 111  
 QY 120 MDYVYVRLSEHGHLVCTSVNLTSTVSLVSNALLAIAIDRYLAIVHPLRPMKQTA 179  
 DB 112 LTYTLNGE--WKMGVPLCHLVPAQGLAVQVSTITLTVALDRHRCIVYHLESKISKRS 169  
 QY 180 TGLIALVMTYSILIAIPSAFTTETVLVIVKSOEKIFCGQIWPVDOQLYYKS-YFLFIFG 238  
 DB 170 FLITGLAMGISALLASPLAIFREYSLEIIPDFEIVACTEKWPEEGEKSQVTVYSLTLL 229  
 QY 239 IEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRRTKTLVLMCILTAIVYLCWA 298  
 DB 230 ILVYPLGIISFSYTRISKLKHNHVSQAADSHYHQR---RHQTKMLVCVVVFAVSWL 286  
 QY 299 PFYGTIVRDEFTTVFVKEKHYLTAFYIVECIAMSNMINTLCFVTVKNDTVKYF----- 353  
 DB 287 PLHAFQLAVIDSHV-LDLKEYKLIETVFHIIAMCSTFANPLLYGWNNSYKRAFLSAFR 345  
 QY 354 --KKIMLLHWKASYNGCKSSADLDLK 377  
 DB 346 CEORLDAIHSEVSMT-FRAKKNLEVK 370  
  
 RESULT 6  
 NY2R\_HUMAN  
 ID NY2R\_HUMAN STANDARD; PRT; 381 AA.  
 AC Q49146; Q13281; Q13457; Q90E67;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).





Db 329 NSNYKAF 336

## RESULT 7

TLR2\_DROME STANDARD; PRT; 519 AA.

AC P30975;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DE 01-JUL-1993 (Rel. 26, Last annotation update)

DE Tachykinin-like peptides receptor 99D (dtkr).

GN TAKR99D.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S;

RX MEDLINE=92007772; PubMed=1717263;

RA Li X.-J., Wolfgang W., Wu Y.-N., North R.A., Forte M.;

RT "Cloning, heterologous expression and developmental regulation of a

RT Drosophila receptor for tachykinin-like peptides.";

RL EMBO J. 10:3221-3229(1991).

CC -1- FUNCTION: PROBABLE RECEPTOR FOR TACHYKININ-LIKE PEPTIDES.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC HIGHEST TO OTHER TACHYKININS RECEPTORS.

CC

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CC -----

CC EMBL; X62711; CAA44595.1; -

CC F1R; S17783; S17783.

CC FlyBase; FBgn0004622; Takr99D.

CC InterPro; IPR000276; GPCR\_Rhodpsn.

CC Pfam; PF00001; 7tm.1.1

CC PRINTS; PR00237; GPCRHOOPS.

CC PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1.

CC PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;

KW Palmitate.

KW

FT DOMAIN 1 100 EXTRACELLULAR (POTENTIAL).

FT TRANSNEM 101 123 1 (POTENTIAL).

FT DOMAIN 124 134 CYTOPLASMIC (POTENTIAL).

FT TRANSNEM 135 155 2 (POTENTIAL).

FT DOMAIN 156 175 EXTRACELLULAR (POTENTIAL).

FT TRANSNEM 176 197 3 (POTENTIAL).

FT DOMAIN 198 217 CYTOPLASMIC (POTENTIAL).

FT TRANSNEM 218 238 4 (POTENTIAL).

FT DOMAIN 239 270 EXTRACELLULAR (POTENTIAL).

FT TRANSNEM 271 292 5 (POTENTIAL).

FT DOMAIN 293 324 CYTOPLASMIC (POTENTIAL).

FT TRANSNEM 325 346 6 (POTENTIAL).

FT DOMAIN 347 361 EXTRACELLULAR (POTENTIAL).

FT TRANSNEM 362 384 7 (POTENTIAL).

FT DOMAIN 385 519 CYTOPLASMIC (POTENTIAL).

FT TRANSNEM 471 481 GLY/SER-RICH.

FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 174 254 BY SIMILARITY.

FT LIPID 399 399 PALMITATE (POTENTIAL).

SQ SEQUENCE 519 AA; 58480 MW; CACC51F50BE476B CRC64;

Query Match 18.9%; Score 387.5; DB 1; Length 519;

Best Local Similarity 27.28; Pred. No. 1.7e-20;

Matches 113; Conservative 82; Mismatches 148; Indels 73; Gaps 18;

QY 1 METTMGFMD-----NATNTST-----SFLSVLN--PHGATATSPFF---NF 37

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1 MENRSDFEADDYGDIDSWSNNSNWSNTPAGVLFSAMSSSVLSASNETPCRTLARSSPYPPVSF 60

QY 38 SYS---DYDMPL-----DEDEDV-----TNSRFEA---AKIVIGHALVYGLVCGIGNF 81

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 61 NHSQTLSTQDPAGVDVEDAAEDAAASNETGSFAPVPMNQVLWSILFGGMVIVATGGNL 120

QY 82 IFTAAALVYRKRLNLTLLIANLAISDFVAIVCCPFEMDYVYVYVQLSWEHGHVLCISVN 141

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 121 IVMIVMTTKRMRTVTNFFVNLISADAVYSSLVNF--NYVYMLSDWPFGEFYCKLSQ 178

QY 142 YLRVSLVSTNALLAIDRYLAIVHPLPRMKQQTATGLIALVWTVSILIAIPSAFT 201

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 179 FIAMLSICASVFTLMAISIDRYVAIRPLQPRSKRCNTAAIAAVIWLASTLSCP----- 233

QY 202 TETVLVIVKSOE-----KIFCGQIW---PVDQQLYKRSYFLFIEFGIEFGVPTVMTL 250

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 234 ---NMIIYRTEVPYRGLSNRTVCYPMPOGPNHSTMESLYNIIILTYFLPIVSMTV 290

QY 251 CYARISRELWPKAVPGQTEQIRKRLCRKTKVLMCLITAYVLCWAPYGFIVRDFE 310

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 291 TYSRVGIELWGSKTIGECTPROVENRSRRVVMIVVYVLIFAICWLPFHSFYIITSY 350

QY 311 PTV---FVKEKHVLTAFYIECIANSMSNITLCFTVVKNDTVKY-FKKIMLLHW 361

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 351 PAITEAPFIQEL-YLAIW-----LANSNSMINPIIYCYM-NSRFYGRF--NVRFRW 398

## RESULT 8

NY2R\_MACMU

ID NY2R\_MACMU STANDARD; PRT; 381 AA.

AC O9GK74;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).

GN NPY2R.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21184974; PubMed=11287088;

RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,

RA Gadenhelmer S., Johnson D., Beavers L.S., Gadsby R.A., Baez M.;

RT "Cloning and characterization of Rhesus monkey neuropeptide Y receptor

RT subtypes.";

RL Peptides 22:343-350(2001).

CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC HIGHEST TO TACHYKININS RECEPTORS.

CC -----

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CC -----

CC EMBL; AF303090; AAG40772.1; -

CC InterPro; IPR000276; GPCR\_Rhodpsn.

CC Pfam; PF00001; 7tm.1.1;

CC PRINTS; PR00237; GPCRHOOPS.

CC PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.

CC PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.

CC

KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 50 72 1 (POTENTIAL).  
 FT DOMAIN 73 82 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 83 104 2 (POTENTIAL).  
 FT DOMAIN 105 124 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 125 146 3 (POTENTIAL).  
 FT DOMAIN 147 166 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 167 187 4 (POTENTIAL).  
 FT DOMAIN 188 214 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 215 240 5 (POTENTIAL).  
 FT DOMAIN 241 268 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 269 291 6 (POTENTIAL).  
 FT DOMAIN 292 304 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 305 328 7 (POTENTIAL).  
 FT DOMAIN 329 381 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 123 203 BY SIMILARITY.  
 FT LIPID 342 342 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 381 AA; 42729 MW; D689D691DC05A49D CRC64;

Query Match 18.78; Score 384.5; DB 1; Length 381;  
 Best Local Similarity 29.28; Pred. No. 2.1e-20;  
 Matches 90; Conservative 74; Mismatches 137; Indels 7; Gaps 4;  
 Qy 47 DEEDVTSRTFFAAKIVIGMALVGMVCGIGNFIFIAALVRYKKLRNLTLNLIANLAI 106  
 Db 35 DPEPLIDSKLIEVQVVLILAYCSILLGVIGNSLVHVVKFSKRTVTNFFIANLAV 94  
 Qy 107 SDFELIVCCPFEMDYVYVYVQLSWHGHVLTCSVNYLRTVSLVYSTNALLAIAIDRYLAI 166  
 Db 95 ADLVVNTLCPLFTLTYYTLGME--WKMGVPLCHLVPAQGLAVQVSTTLTVALDRHRCI 152  
 Qy 167 VHLPRPMKOTAGLALVYVTSILTAIPSAFTTETVLVYKSKIECGIWPVDQO 226  
 Db 153 VYHLESKISRISPLIIIGLWAGISALLASPLAIFREYSLEIIPDFEIVACTEKWPGEEK 212  
 Qy 227 -LYKSYFLFIEFGVGVVYVMTLCYARISRELWFKAVPGFOTEQIRKRLCRKRTVLV 285  
 Db 213 SIYGVTVSLSLLLLYLVPLGIIISFYSYTRISKLKSHVSPGANDHYHQ--RQKTKM 269  
 Qy 286 LMCILTAIVLCWAFYGTIVRDPFFTVFKKHYLTAIFYECIAMSNSMINTLCFTVY 345  
 Db 270 LVCVVVFAVSWLPLHAFQALAVDIDSHV-LDLKEYKLFTVTHIAMCSFANPLLYGWM 328  
 Qy 346 KNDYVKVF 353  
 Db 329 NSNRKAF 336

## RESULT 9

NY2R\_CAVPO  
 ID NY2R\_CAVPO STANDARD; PRT; 381 AA.  
 AC Q942D5;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Neuropeptide Y receptor type 2 (NPY-2) (NPY-Y2 receptor).  
 GN NPY2R.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99017376; PubMed=9802390;  
 RX Sharma P.S., Holmberg S.K., Eriksson H., Beck-Sickinger A.G.,  
 RA Grundemar L., Larhammar D.;  
 RT "Cloning and functional expression of the guinea pig neuropeptide Y  
 RT Y2 receptor."  
 RL Regul. Pept. 75:23-28(1998).  
 CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO TACHYKININS RECEPTORS.  
 CC  
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 CC  
 CC EMBL; AF072821; AAD13143.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1.1.  
 DR PRINTS; PRO0237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECP\_FL\_1.1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECP\_FL\_2.1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 51 73 1 (POTENTIAL).  
 FT DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 84 105 2 (POTENTIAL).  
 FT DOMAIN 106 125 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 126 147 3 (POTENTIAL).  
 FT DOMAIN 148 167 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 168 188 4 (POTENTIAL).  
 FT DOMAIN 189 215 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 216 241 5 (POTENTIAL).  
 FT DOMAIN 242 269 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 270 292 6 (POTENTIAL).  
 FT DOMAIN 293 305 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 306 329 7 (POTENTIAL).  
 FT DOMAIN 330 381 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 124 204 BY SIMILARITY.  
 FT LIPID 343 343 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 381 AA; 42332 MW; D806B859A43ECACE CRC64;

Query Match 18.48; Score 379; DB 1; Length 381;  
 Best Local Similarity 27.98; Pred. No. 5.1e-20;  
 Matches 98; Conservative 79; Mismatches 158; Indels 16; Gaps 6;  
 Qy 5 MGFMDNATNTSFLSVLNPHG-AHATSPFNFSYSDYMDPLDEDEDVTSRTFFAAKI 63  
 Db 1 MGPIGTEADENQVVEIKVEPYGPGHTT-----PRGELAPDPPELIDSKLTVRV 52  
 Qy 64 VIGMALVGMVCGIGNFIFIAALVRYKKLRNLTLNLIANLAIISDFLVAIVCCPFEMDY 123  
 Db 53 VLILAYCSIILLGVVGNLSLVHVVKFSKRTVTNFFIANLAVADLLVNTLCPLFTLT 112  
 Qy 124 VVQLSWHGHVLTCSVNYLRTVSLVYSTNALLAIAIDRYLAVHPLRPMKQOTATGLI 183  
 Db 113 LMGE--WKMGVPLCHLVPAQGLAVQVSTTLTVALDRHRCIVYHLDKISKQNSFLII 170  
 Qy 184 ALVMTVSILTAIPSAFTTETVLVYKSKIECGIWPVDQO-LYKSYFLFIEFGVY 242  
 Db 171 GLWAGISALLASPLAIFREYSLEIIPDFEIVACTEKWPGEEKSIYGVYSLSSLLIVY 230  
 Qy 243 GPVVTWTLCYARISRELWFKAVPGFOTEQIRKRLCRKRTVLVLMCILLTAIVLCWAFY 302  
 Db 231 LPLGIISVSVYRISWKLKNSHVSPGANDHYHQ---RQKTKGLVTVVVVFAVSWLPLHA 287  
 Qy 303 FTIVRDPFFTVFKKHYLTAIFYECIAMSNSMINTLCFTVTVKNDYVKVF 353  
 Db 288 FQLAVIDSQV-LDLKEYKLFTVTHIAMCSFANPLLYGNNSYRKAF 337  
 RESULT 10  
 GP10\_HUMAN  
 ID GP10\_HUMAN STANDARD; PRT; 370 AA.  
 AC P49683; O75194;

DT 01-FEB-1996 (Rel. 33, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Proactin-releasing peptide receptor (PrRP receptor) (PrRP) (G protein-coupled receptor GPR10) (hGR3).

GN GPR10 OR GR3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96115583; PubMed=8666380;

RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R., Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R., O'Dowd B.F., Docherty J.M.;

RA "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10, and GPR14, encoding receptors related to interleukin 8, neuropeptide Y, and somatostatin receptors.";

RT Y, and somatostatin receptors.";

RL Genomics 29:335-344(1995).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98268781; PubMed=9607765;

RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;

RA "A prolactin-releasing peptide in the brain.";

RL Nature 393:272-276(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA Ozawa A., Yamada M., Sato T., Monden T., Hashimoto K., Sasaki T., Mori M.;

RA "Transcriptional regulation of the human prolactin-releasing peptide (PrRP) receptor gene by a dopamine agonist.";

RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RN TISSUE SPECIFICITY

RX MEDLINE=99426652; PubMed=10498338;

RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M.;

RA "Tissue distribution of prolactin-releasing peptide (PrRP) and its receptor.";

RT Regul. Pept. 83:1-10(1999).

RL CC -1- FUNCTION: Receptor for prolactin-releasing peptide (PrRP).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Only detected in the pituitary gland.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U32672; AAC50504.1; ..

DR EMBL: AB015745; BAA31159.1; ..

DR EMBL: AB048946; BAB83030.1; ..

DR Genew: HGNC:4464; GPR10.

DR MIM: 60895; ..

DR GO: GO:0005887; C: integral to plasma membrane; TAS.

DR GO: GO:0008188; F: neuropeptide receptor activity; TAS.

DR GO: GO:0007186; F: G-protein coupled receptor protein signalin...; TAS.

DR GO: GO:0007565; P: pregnancy; TAS.

DR InterPro: IPR000276; GPCR\_Rhodpsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR\_Rhodopsin.

DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.

DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 63 83 1 (POTENTIAL).

FT DOMAIN 84 101 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 102 122 2 (POTENTIAL).

FT DOMAIN 123 126 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 127 147 3 (POTENTIAL).

FT DOMAIN 148 175 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 176 196 4 (POTENTIAL).

FT DOMAIN 197 225 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 226 246 5 (POTENTIAL).

FT DOMAIN 247 276 6 (POTENTIAL).

FT TRANSMEM 277 297 7 (POTENTIAL).

FT DOMAIN 298 317 8 (POTENTIAL).

FT TRANSMEM 318 338 9 (POTENTIAL).

FT DOMAIN 339 369 10 (POTENTIAL).

FT DISULFID 370 411 11 (POTENTIAL).

FT CARBOHYD 372 411 12 (POTENTIAL).

FT CARBOHYD 373 411 13 (POTENTIAL).

FT CONFLICT 89 175 RISLR -> ASRCA (IN REF. 1).

FT CONFLICT 170 194 A -> P (IN REF. 1).

FT CONFLICT 194 194 A -> P (IN REF. 1).

SQ SEQUENCE 370 AA; 41106 MW; 08E9E57FBE6FC809 CRC64;

Query Match 18.08; Score 370; DB 1; Length 370;

Best Local Similarity 28.5%; Pred. No. 2.2e-19; Mismatches 144; Indels 34; Gaps 13;

Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;

QY 21 SVLNPHGABATSPFNFSYSDYMDPLDEDEDVTSRTFFAAKIVIGM--ALVIGIMLVCG- 77

DB 21 AVTTPNQSAEASAGSGSVAGADAPA-----VTFQSLQLVHQLGLVLLYSVVVGL 75

QY 78 IGNTFTALRYKKLNLTNLIANLAISDFLVAIVCCPFMDYVYVROLSEHSHVLC 137

DB 76 VGNCLLVLTARVRLHNVTFNLGNLSDVLMCTACVPLTL-AYAFEPGVVGGGLC 134

QY 138 TSVNKLRTSVLSYVSTNALLAIDRYLAIVHPRMKCOTATGLIALVWTSILIAIPS 197

DB 135 HUVFLQPVTVVSVFTLTITVDRVTVVHPLRRISLSLRSAYAVLAINALSVALPA 194

QY 198 AYFTTETVLIVKQKIFGQIPVDQ---QLYKSYFLFIFGIEFVGPVVTMTLCYAR 254

DB 195 A---VHTYHVELKPHDVLRCLEEFQSGOERQQLYAWGLL---VTYLLPLVLLSYVR 247

QY 255 ISRELKFAVPGFQTEQIRKRLC-REKTVLVLWCILTAVLCAWPGYGTIVRDFPTV 313

DB 248 VSVKLRNVPGCVTQSQADWDARRRTFCLLVVVVVVAVCVMLPHVFNLLRLDLP-- 305

QY 314 FVREKHYLT--AFYIVE--C--IAMSMTINTLCFTVTKNDTVKFKIMLLHW 361

DB 306 -----HAIDPVAFGLVQLLCHLWLAASACYNPFYAML-HDSFREELKLLVAW 353

RESULT 11

GP10\_RAT

ID GP10\_RAT

AC Q64121

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Proactin-releasing peptide receptor (PrRP receptor) (PrRP) (G protein-coupled receptor GPR10) (UHR-1).

GN GPR10.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE=Hypothalamus;

RX MEDLINE=95251659; PubMed=7733930;

RA Welch S.K., O'Hara B.F., Kilduff T.S., Heller H.C.;

RT "Sequence and tissue distribution of a candidate G-coupled receptor cloned from rat hypothalamus.";

RL Biochem. Biophys. Res. Commun. 209:606-613(1995).

RN [2]  
 RX TISSUE SPECIFICITY.  
 RA MEDLINE-99426652; PubMed-10498338;  
 RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,  
 RA Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,  
 RA Sumino Y., Fujino M.;  
 RT "Tissue distribution of prolactin-releasing peptide (PrRP) and its  
 receptor";  
 RL Regul. Pept. 83:1-10(1999).  
 CC -!- FUNCTION: Receptor for prolactin-releasing peptide (PrRP).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in  
 CC pituitary, cerebellum, and hypothalamus.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 DR EMBL; S77867; AB34129.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00237; G-PROTEIN\_RECP\_FL\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 62  
 FT TRANSSEM 63 83  
 FT DOMAIN 84 101  
 FT TRANSSEM 102 122  
 FT DOMAIN 123 126  
 FT TRANSSEM 127 147  
 FT DOMAIN 148 175  
 FT TRANSSEM 176 196  
 FT DOMAIN 197 223  
 FT TRANSSEM 224 244  
 FT DOMAIN 245 276  
 FT TRANSSEM 277 297  
 FT DOMAIN 298 317  
 FT TRANSSEM 318 338  
 FT DOMAIN 339 370  
 FT DISULFD 134 211  
 FT CARBOHYD 27 27  
 FT CARBOHYD 36 36  
 FT SEQUENCE 370 AA; 41160 MW; 8E5E5689D127CB2C CRC64;  
 Query Match 17.9%; Score 367.5; DB 1; Length 370;  
 Best Local Similarity 30.1%; Pred. No. 3.3e-19;  
 Matches 91; Conservative 67; Mismatches 121; Indels 23; Gaps 10;  
 QY 69 LVGIMLVCG-IGNFIFIAALVYKRLNLTLLIANLAISDFLVAIVCCPEMDYVYVYRQ 127  
 DB 66 LYSIVVYVGLVGNCLLVIAVRVRLHNTNFIIGNLALSDFVLMCAACVPLT-AYAFEP 124  
 QY 128 LSWEHGHLCTSVNLYRTVSVLSTNALLAIDRYLAIVHPRLMKCQATGLIALVW 187  
 DB 125 RQWFGGGLCHLVFLPQVTVVSVFTLTAVDRVYVVLVPLRRISLKLAVYVIGW 184  
 QY 188 TVSILIAIPSYFTTETVLVIVKSEKIFCGQIPVDQOLYKSYFLFIFGI---EFVGP 244  
 DB 185 ALSAVLALPAA---VHTYHVELKPHDVLCEEFNGSQE---RQRIYAWGLLLGTLLP 237  
 QY 245 VVTWTLCTVARSRELWFAVFGFQTEQTKRLRC-RRRTVLVLMCLTAYVLCWAPFVG 303  
 DB 238 LLAILLTVRSVSKLRNRPVGSVTSQADWDRAARRRTFCLLVVVVVVFVLCWPLHIF 297  
 QY 304 TIVRDFEPTVFKRHYLTAFFIVE--C--TAMSNMINTLCFVTKNDYVYKFKIMLL 359  
 DB 298 NLRLDLPRAIDP-----YAFGLVQLCHWLAHSSACTNPFIYAWL-HDSPRELRKMLL 351

QY 360 HW 361  
 DB 352 SW 353  
 RESULT 12  
 NK2R\_MOUSE STANDARD; PRT; 384 AA.  
 ID NK2R\_MOUSE  
 AC P30549; 1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Substance-K receptor (SKR) (Neurokinin A receptor) (NK-2 receptor)  
 DE (NK-2R).  
 GN TACR2 OR TAC2R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Intestine;  
 RX MEDLINE-92137253; PubMed-1370937;  
 RA Sundelin J.B., Provvedini D.M., Wahlestedt C.R., Laurell H.,  
 RA Pohl J.S., Peterson P.A.;  
 RT "Molecular cloning of the murine substance K and substance P receptor  
 RT genes";  
 RL Eur. J. Biochem. 203:625-631(1992).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE  
 CC SUBSTANCE K (NEUROKININ A). IT IS ASSOCIATED WITH G PROTEINS THAT  
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO  
 CC TACHYKININS IS: SUBSTANCE K > NEUROMEDIN K > SUBSTANCE P.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO OTHER TACHYKININS RECEPTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; X62933; CAA44706.1; -;  
 DR PIR; S20303; S20303.  
 DR HSP; P02699; I1F88.  
 DR MGD; MGI:98477; Tacr2.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00237; G-PROTEIN\_RECP\_FL\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 32  
 FT TRANSSEM 33 56  
 FT DOMAIN 57 69  
 FT TRANSSEM 70 90  
 FT DOMAIN 91 107  
 FT TRANSSEM 108 129  
 FT DOMAIN 130 149  
 FT TRANSSEM 150 170  
 FT DOMAIN 171 196  
 FT TRANSSEM 197 218  
 FT DOMAIN 219 251  
 FT TRANSSEM 252 272  
 FT DOMAIN 273 290  
 FT TRANSSEM 291 310  
 FT DOMAIN 311 384  
 FT CARBOHYD 11 11  
 N-LINKED (GLCNAC...) (POTENTIAL).

```

FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 181 BY SIMILARITY.
FT LIPID 324 324 PALMITATE (POTENTIAL).
SQ SEQUENCE 384 AA: 43114 MW: 7937F05A2BB90759 CRC64;

Query Match 17.7%; Score 363; DB 1; Length 384;
Best Local Similarity 27.0%; Pred. No. 7e-19;
Matches 93; Conservative 69; Mismatches 136; Indels 46; Gaps 9;

QY 8 MDONATNTSFLSVLPHGHAHATSPFFNEFSYSDYDMPDLEEDVNTSRTFFAAKIVIGM 67
DB 1 MGAHASVTDNTNLSGLSNAATGVTGTA-----FSMPGWQLAL-----WAT 38
QY 68 ALVGLMVCVGGIFGFIPTAALVRKLLRNLTNLIANLAIISDFLVAIVCCPFEMDYVVVRQ 127
DB 39 AYALVLVAVTGATVNIWIILAHERTVNTYFIINLALADLCMAAFNATFNFIY--ASH 96
QY 128 LSWEHGHVLCVTSNYLRTSVLYSTNALLAIAIDRYLAIVHPLRPKQCOTATGLIALVM 187
DB 97 NIWTFGSTFCYFQNLFPVTAMFVSIYSMTAIAADRYMAIVHPPRLSAPSTKAVIAVIM 156
QY 188 TVSLIIAIPSNAYETTERVLIVKSOEKFICGQIWPVDO-----QLYKSYELFIFGIEFV 242
DB 157 LVALLALASPOCFYSTIV-----DQGATKCVWAPNDNGKMLLLHLVVFVLIYEL--- 208
QY 243 GPVVVMTCLYARISRELWFKAVPFGFQEQIRKR-LRCRRKRTVLVLMCIITAYVLCWAPFY 301
DB 209 -PLVWMPAAVSVIGLTLWRAVPRHQAGANLRLQAKKFKVAMVLVVVTFPAICWLPYH 267
QY 302 GFTIVRDFFTVFKV-----EKHYLTAFYIVECIAMSNMINTLCF 342
DB 268 LYFILGTQEDYVYRKFIQOYVLALEF-----LAMSTMYNPIIY 307

RESULT 13
NKLR_RAT STANDARD; PRT; 407 AA.
AC PI4600;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
GN TACR1 OR TACR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91154239; PubMed=1705552;
RA Hershey A.D., Dykema P.E., Krause J.E.;
RT *Organization, structure, and expression of the gene encoding the rat
RT substance P receptor.*;
RL J. Biol. Chem. 266:4366-4374(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036822; PubMed=2478537;
RA Yokota Y., Sasai Y., Tanaka K., Fujiwara T., Tsuchida K.,
RA Shigemoto R., Kakizuka A., Ohkubo H., Nakanishi S.;
RT *Molecular characterization of a functional cDNA for rat substance P
RT receptor.*;
RL J. Biol. Chem. 264:17649-17652(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=90161991; PubMed=2154852;
RA Hershey A.D., Krause J.E.;
RT *Molecular characterization of a functional cDNA encoding the rat
RT substance P receptor.*;
RL Science 247:958-962(1990).
RN [4]
RP REVISION TO 213.
RP STRAIN=Sprague-Dawley;
RC

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RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC !- SUBCELLULAR LOCATION: Integral membrane protein.
CC !- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
CC TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M64236; AAA42176.1; -.
DR EMBL: M64232; AAA42176.1; JOINED.
DR EMBL: M64233; AAA42176.1; JOINED.
DR EMBL: M64234; AAA42176.1; JOINED.
DR EMBL: M64235; AAA42176.1; JOINED.
DR EMBL: J05097; AAA42175.1; -.
DR EMBL: M31477; AAB59726.1; -.
DR PIR: A38692; A34357.
DR InterPro: IPR000276; GPCR_Rhodosp.
DR Pfam: PF00001; 7tm_1; 1
DR PRINTS: PRO0237; GPCRHHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 54 1 (POTENTIAL).
FT DOMAIN 55 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 128 3 (POTENTIAL).
FT DOMAIN 129 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 219 5 (POTENTIAL).
FT DOMAIN 220 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 308 7 (POTENTIAL).
FT DOMAIN 309 407 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 105 180 BY SIMILARITY.
FT LIPID 322 322 PALMITATE (POTENTIAL).
FT CONFLICT 73 73 N -> D (IN REF. 3).
SQ SEQUENCE 407 AA; 46366 MW; ADF85A0BF551C96 CRC64;

Query Match 17.6%; Score 362.5; DB 1; Length 407;
Best Local Similarity 25.5%; Pred. No. 8e-19;
Matches 82; Conservative 84; Mismatches 129; Indels 27; Gaps 10;

QY 41 DYDMPDLEED-----EDVNTSRTFFAA--KIVIGALVGMVCC-IGNFIFIAALVRYK 91
DB 2 DNVLPMSDLFPNISTNTSESQFQPTQWIVLMAAAYTVIVTSVGVNVVILAHK 61
QY 92 KLRNLTNLIANLAIISDFLVAIVCCPFEMDYVVVRQLSWEHGHVLCVTSVNLRTSVLYVS 151
DB 62 RKRVTNVTFLVNLAFACMAAFNTVNTAV--HNWYIGLFYCKFHFPIAALFAS 119
QY 152 TNALLAIAIDRYLAIVHPLRPKQCOTATGLIALVWTVSILIAIPSAFY-TTETVLVIVK 210
DB 120 IYSMTAVAFDRYMAIHPQLRSLATATKVIWFLVALLAFPGGYSTETM----- 174
QY 211 SOEKIFCGQIWPV-DQQLYKSYFLFIFGIEFVGPVVTMLCYARISRELWFKAVPFGQT 269

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Db 175 -PSRVVCMIEPHEPNRTYKAYHICVTLVLYFLPLVIGYAVTWGTLWASIPGDS 233
Qy 270 EQIKRLRCRKTVLVMCLITAVLWCHAPPGYFTIVRDFPTVFK---EKHYLTAFYI 326
Db 234 DRYHEQYSAKRYKVMVIVVCTFAICWLPFHVFFLLPYNPDLYLKFKFQOQVYLSMW- 292
Qy 327 VECIAMSNTLCFVTVKND 348
Db 293 ---LAMSTWYNPIIYCL-ND 310

RESULT 14
NK1R_MOUSE
ID NK1R_MOUSE STANDARD; PRT; 407 AA.
AC P30548;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
GN TACR1 OR TAC1R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=92137253; PubMed=1370937;
RA Sundelin J.B., Provvedini D.M., Wahlestedt C.R., Laurell H.,
RA Pohl J.S., Peterson P.A.;
RT "Molecular cloning of the murine substance K and substance P receptor
RT genes.";
RL Eur. J. Biochem. 203:625-631(1992).
RN [2]
RP SEQUENCE OF 53-290 FROM N.A.
RC STRAIN=CBA; TISSUE=Brain, and T-cell;
RX MEDLINE=94165478; PubMed=8120392;
RA Cook G.A., Elliott D., Metwalli A., Blum A.M., Sandor M., Lynch R.,
RA Weinstein J.V.;
RT "Molecular evidence that granuloma T lymphocytes in murine
RT schistosomiasis mansoni express an authentic substance P (NK-1)
RT receptor.";
RL J. Immunol. 152:1830-1835(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
CC TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62934; CAA44707.1; -
DR EMBL; L27828; AAA17892.1; -
DR EMBL; L27826; AAA17891.1; -
DR PIR; S20304; S20304.
DR MGD; MGI:98475; Tacrl.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.

```

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FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 54 1 (POTENTIAL).
FT DOMAIN 55 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 128 3 (POTENTIAL).
FT DOMAIN 129 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 219 5 (POTENTIAL).
FT DOMAIN 220 248 6 (POTENTIAL).
FT TRANSMEM 249 270 7 (POTENTIAL).
FT DOMAIN 271 283 8 (POTENTIAL).
FT TRANSMEM 284 308 9 (POTENTIAL).
FT DOMAIN 309 407 10 (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 105 180 BY SIMILARITY.
FT LIPID 322 322 PALMITATE (POTENTIAL).
SQ SEQUENCE 407 AA; 451B6D475A6659A0 CRC64;

Query Match 17.5%; Score 360.5; DB 1; Length 407;
Best Local Similarity 25.5%; Pred. No. 1.1e-18;
Matches 82; Conservative 84; Mismatches 129; Indels 27; Gaps 10;

Qy 41 DYDMLDED-----EDVTNSTRFFAA--KIVIGMALVIGIMLVCG-IGNFIFTAALVRVK 91
Db 2 DNVLPVDSLDLPNTSTNTSESQFQVQWQIVLWAAAYVIVTVSVGVNVMVWIIAHLK 61
Qy 92 KLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVVRQLSMEHGHVLTCSVNYLRTSLYVS 151
Db 62 RMRVTNIVFLVNLAFACAAFAETVNVFTYAV--HNVVYGLFYCKFHNFFPFAALFAS 119
Qy 152 TNALLAIDRYLAIVHPLRPMKQATATGLIALVWTVSILIALPSAYF-TTETVLVYVK 210
Db 120 IYSMTAVAFQRYMAIHPQPLRSATATKVIVFWLALLAFPOGYSTTETM----- 174
Qy 211 SOBKIIFGQIWPV-DQOLYKSYFLFIEFGYFVGVVMTLCYARISRELWKAIVPGFOT 269
Db 175 -PSRVVCMIEPHEPNRTYKAYHICVTLVLYFLPLVIGYAVTWGTLWASIPGDS 233
Qy 270 EQIKRLRCRKTVLVMCLITAVLWCHAPPGYFTIVRDFPTVFK---EKHYLTAFYI 326
Db 234 DRYHEQYSAKRYKVMVIVVCTFAICWLPFHVFFLLPYNPDLYLKFKFQOQVYLSMW- 292
Qy 327 VECIAMSNTLCFVTVKND 348
Db 293 ---LAMSTWYNPIIYCL-ND 310

RESULT 15
NK2R_RABIT
ID NK2R_RABIT STANDARD; PRT; 384 AA.
AC P79218;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Substance-K receptor (SKR) (Neurokinin A receptor) (NK-2 receptor)
DE (NK-2R).
GN TACR2 OR TAC2R.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pulmonary artery;
RX MEDLINE=95182423; PubMed=7877137;
RA Aharony D., Little J., Thomas C., Powell S., Downey-Jones M.,
RA Graham A.;
RT "Isolation and characterization of neurokinin A receptor cDNAs from
RT guinea-pig lung and rabbit pulmonary artery.";
RL J. Recept. Res. 14:399-421(1994).

```

```

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE K (NEUROKININ A). IT IS ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC -----
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CC -----
DR EMBL: S82448; BAB46747.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1;
DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2;
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 33 56 1 (POTENTIAL).
FT DOMAIN 57 69 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 70 90 2 (POTENTIAL).
FT DOMAIN 91 107 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 150 170 4 (POTENTIAL).
FT DOMAIN 171 196 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 197 218 5 (POTENTIAL).
FT DOMAIN 219 251 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 252 272 6 (POTENTIAL).
FT DOMAIN 273 290 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 291 310 7 (POTENTIAL).
FT DOMAIN 311 384 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 181 BY SIMILARITY.
FT LIPID 324 324 PALMITATE (POTENTIAL).
SQ SEQUENCE 384 AA; 43127 MW; F35850DF224BF9E9 CRC64;
Query Match 17.48; Score 358; DB 1; Length 384;
Best Local Similarity 28.58; Pred. No. 1.6e-18;
Matches 81; Conservative 63; Mismatches 116; Indels 24; Gaps 7;
Qy 68 ALVGIMLVCGIGNFIFTAALVRYKKLNLLIANLAISDFVAIVCCPFEMDYVYVRQ 127
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 39 AYALVLVAVVGNAVTVIILAHRRMTVTVNYFTVNLADLCMTAFNAFNFVY--ASH 96
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 128 LSWEGHVLCTSVNYLRTSVLYXVSTNALLAIDRYLAIVHPLRPMCKQTATGLIALVW 187
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 97 NIWYFGAFYFQNLFFITAMFVSIYKSTALADRYMAIVHPQPRLSGGCTKAVIAGIW 156
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 188 TVSLIIAIPSAFTTETVVLVIVKSKQIFGQIWPVQ-----QLYKYSFLFIIGIEFY 242
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 157 LVALALAFQCFYST-----ITMDQGATKCVAMPEDSGGKMLLYHLTVIALIYFL--- 208
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 243 GPVVTWTLGVARISRELWEKAVPQEPQEQIKR-LRCRRKTVLVMCLITAYVLCWAPFY 301
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 209 -PLVVMFVAVSGFKLRRRTVPQHOTGANRLRAKKRFVKYTWLVVTVTFVAVCWLPYH 267
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 302 GFTIVRDFPFPVFK-----EKHYLPAFTVIECIAMNSMINTLCF 342
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 268 LYFLIGHFQDDIGCKRTIQOQVLLFW-----LAMSSTMYNPDIY 307
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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Search completed: October 7, 2003, 09:50:57  
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:50:42 ; Search time 20 Seconds  
(without alignments)  
831.408 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 MTTMGPMDDNATNTSTSL.....LDLKTICMPATEVDCIRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 1766  | 85.9        | 384    | 2     | US-08-833-226-2    |
| 2          | 401.5 | 19.5        | 381    | 2     | US-08-687-355A-4   |
| 3          | 401.5 | 19.5        | 381    | 4     | US-09-407-367-4    |
| 4          | 395.5 | 19.2        | 381    | 2     | US-08-687-355A-6   |
| 5          | 395.5 | 19.2        | 381    | 4     | US-09-407-367-6    |
| 6          | 387.5 | 18.9        | 381    | 1     | US-08-192-288-2    |
| 7          | 387.5 | 18.9        | 381    | 2     | US-08-687-355A-2   |
| 8          | 387.5 | 18.9        | 381    | 4     | US-09-200-673-16   |
| 9          | 387.5 | 18.9        | 381    | 4     | US-09-407-367-2    |
| 10         | 384.5 | 18.7        | 381    | 4     | US-08-876-798A-2   |
| 11         | 370   | 18.0        | 370    | 3     | US-08-513-974B-26  |
| 12         | 370   | 18.0        | 370    | 3     | US-08-513-974B-323 |
| 13         | 370   | 18.0        | 370    | 3     | US-09-172-353-5    |
| 14         | 370   | 18.0        | 370    | 3     | US-08-776-971-21   |
| 15         | 370   | 18.0        | 370    | 3     | US-08-776-971-104  |
| 16         | 370   | 18.0        | 370    | 4     | US-09-799-955-5    |
| 17         | 370   | 18.0        | 370    | 4     | US-09-461-436B-26  |
| 18         | 369.5 | 18.0        | 369    | 3     | US-09-172-353-6    |
| 19         | 369.5 | 18.0        | 369    | 4     | US-09-799-955-6    |
| 20         | 369.5 | 18.0        | 369    | 4     | US-09-170-496D-26  |
| 21         | 368.5 | 17.9        | 369    | 4     | US-09-170-496D-178 |
| 22         | 368.5 | 17.9        | 370    | 3     | US-08-776-971-140  |
| 23         | 367.5 | 17.9        | 370    | 3     | US-09-172-353-7    |
| 24         | 367.5 | 17.9        | 370    | 4     | US-09-799-955-7    |
| 25         | 363.5 | 17.7        | 370    | 3     | US-09-172-353-2    |
| 26         | 363.5 | 17.7        | 370    | 3     | US-09-172-353-3    |
| 27         | 363.5 | 17.7        | 370    | 4     | US-09-799-955-2    |

|    |       |      |     |   |                  |                   |
|----|-------|------|-----|---|------------------|-------------------|
| 28 | 363.5 | 17.7 | 370 | 4 | US-09-799-955-3  | Sequence 3, Appli |
| 29 | 362.5 | 17.6 | 372 | 1 | US-07-937-609-20 | Sequence 20, Appl |
| 30 | 362.5 | 17.6 | 372 | 3 | US-08-029-170-20 | Sequence 20, Appl |
| 31 | 362.5 | 17.6 | 407 | 5 | PCT-US92-06532-7 | Sequence 7, Appli |
| 32 | 357.5 | 17.4 | 407 | 2 | US-08-390-000A-6 | Sequence 6, Appli |
| 33 | 356.5 | 17.3 | 311 | 1 | US-07-701-935-26 | Sequence 26, Appl |
| 34 | 356.5 | 17.3 | 407 | 1 | US-08-117-965-26 | Sequence 26, Appl |
| 35 | 356.5 | 17.3 | 407 | 5 | PCT-US92-06532-3 | Sequence 3, Appli |
| 36 | 351   | 17.1 | 402 | 3 | US-08-846-704-4  | Sequence 3, Appli |
| 37 | 351   | 17.1 | 402 | 4 | US-08-462-509B-2 | Sequence 2, Appli |
| 38 | 351   | 17.1 | 402 | 5 | PCT-US95-05616-2 | Sequence 2, Appli |
| 39 | 351   | 17.1 | 425 | 3 | US-08-846-704-2  | Sequence 2, Appli |
| 40 | 351   | 17.1 | 425 | 4 | US-09-479-128-2  | Sequence 2, Appli |
| 41 | 350   | 17.0 | 369 | 4 | US-08-462-509B-4 | Sequence 4, Appli |
| 42 | 350   | 17.0 | 369 | 5 | PCT-US95-05616-4 | Sequence 4, Appli |
| 43 | 350   | 17.0 | 372 | 4 | US-08-462-509B-6 | Sequence 6, Appli |
| 44 | 350   | 17.0 | 377 | 5 | PCT-US95-05616-6 | Sequence 6, Appli |
| 45 | 350   | 17.0 | 389 | 2 | US-08-846-705-2  | Sequence 2, Appli |

ALIGNMENTS

RESULT 1  
US-08-833-226-2  
; Sequence 2, Application US/08833226  
; Patent No. 5891720  
; GENERAL INFORMATION:  
; APPLICANT: Moore, Karen  
; APPLICANT: Nagle, Deborah  
; APPLICANT: Woolf, Elizabeth  
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,226  
; FILING DATE: 17-APR-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-080  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-833-226-2

Query Match 85.9%; Score 1766; DB 2; Length 384;

Best Local Similarity 87.4%; Pred. No. 1.5e-168;

Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 12 ATNTSTSLSPNPGAHATSPFNFSYSDYDMPLEDEDYNTSTFFAAKIVIGALVG 71

DB 3 AQNGTSTFTPNFPDQDHASSLSFNFGYDLPDEDEDYNTSTFFAAKIVIGALVG 62



[illegible]

RESULT 3  
DS-09-407-367-4

```

:
:
: GENERAL INFORMATION:
:
: APPLICANT: Cristophe P.G. Gerald, et al.
:
: TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECI
:
: NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Cooper & Dunham LLP
:
: STREET: 1185 Avenue of the Americas
:
: City: New York
:
:

```

[illegible]



Db 266 MTKMLVCVVVFAVSWLPLHAFQALAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLL 324  
 QY 342 FVTYKNDTVKYF-----KKMLLHWKASVNGKSSADLDX 377  
 Db 325 YGMNSNRYKAFLSAFRCERQRLDAIHSEVSMT-FAKKNLEVK 366

## RESULT 6

US-08-192-288-2  
 ; Sequence 2, Application US/08192288  
 ; Patent No. 5545549  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe  
 ; APPLICANT: Walker, Mary  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Weinshank, Richard L.  
 ; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE  
 ; TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTOR AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/192,288  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 44742/JPW/TEP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 977-9550  
 ; TELEX: 422523 COOP UI  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 381 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-192-288-2

Query Match 18.9%; Score 387.5; DB 1; Length 381;  
 Best Local Similarity 29.5%; Pred. No. 1.1e-30;  
 Matches 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;  
 QY 47 DEDEDVTNSRTFFAAKIVIGMALVGMVCGIGNFTIAALVRYKKRLNLLIANLAI 106  
 Db 35 DPEPLIDSKLEVVQWLILAYCSIIILGVGNSLVHVIWIKFKSMRTVTNFFIANLAV 94  
 QY 107 SDFLVAIVCCPFEMDYVVRQLSWEGHVLCTSVNLTFRVSLVSTNALLAIDRYLAI 166  
 Db 95 ADLLVNTLCPLFTLTLMGE--WKMGPVLCVLPYAQGLAVQVSTITLTVALDRHRCI 152  
 QY 167 VHLPRMKQOTATGLIALVMTVYSILIAIPSAFTTETVLVIVKSOEKFICGQIWPVDOQ 226  
 Db 153 VYHLESKISRISFLIIGLAWGISALLASPLAIFREYSILIEIPDFEIVACTEKWPGEK 212  
 QY 227 -LYKSYFLIFIGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285  
 Db 213 SIYGTVYSLSLILVPLGLIISFSYTRISWKLKNHVSFGAANDRYHQR---RQKTTKM 269  
 QY 227 -LYKSYFLIFIGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285  
 Db 213 SIYGTVYSLSLILVPLGLIISFSYTRISWKLKNHVSFGAANDRYHQR---RQKTTKM 269

QY 286 LMCILTAYVLCNAPYGGFTIVDRFPPTVFRKHKYLTAFYIVECIAMNSMINTLCFTTV 345  
 Db 270 LVCVVVFAVSWLPLHAFQALAVDIDSOV-LDLKEYKLIFTVFHIIAMCSTFANPLLIGWM 328  
 QY 346 KNDTVKYF 353  
 Db 329 NSNYRKAF 336

## RESULT 7

US-08-687-355A-2  
 ; Sequence 2, Application US/08687355A  
 ; Patent No. 5989834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Synaptic Pharmaceutical Corporation  
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE  
 ; TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/687,355A  
 ; FILING DATE: No. 5989834ember 26, 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 381 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-687-355A-2

Query Match 18.9%; Score 387.5; DB 2; Length 381;  
 Best Local Similarity 29.5%; Pred. No. 1.1e-30;  
 Matches 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;  
 QY 47 DEDEDVTNSRTFFAAKIVIGMALVGMVCGIGNFTIAALVRYKKRLNLLIANLAI 106  
 Db 35 DPEPLIDSKLEVVQWLILAYCSIIILGVGNSLVHVIWIKFKSMRTVTNFFIANLAV 94  
 QY 107 SDFLVAIVCCPFEMDYVVRQLSWEGHVLCTSVNLTFRVSLVSTNALLAIDRYLAI 166  
 Db 95 ADLLVNTLCPLFTLTLMGE--WKMGPVLCVLPYAQGLAVQVSTITLTVALDRHRCI 152  
 QY 167 VHLPRMKQOTATGLIALVMTVYSILIAIPSAFTTETVLVIVKSOEKFICGQIWPVDOQ 226  
 Db 153 VYHLESKISRISFLIIGLAWGISALLASPLAIFREYSILIEIPDFEIVACTEKWPGEK 212  
 QY 227 -LYKSYFLIFIGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRTVLV 285  
 Db 213 SIYGTVYSLSLILVPLGLIISFSYTRISWKLKNHVSFGAANDRYHQR---RQKTTKM 269  
 QY 286 LMCILTAYVLCNAPYGGFTIVDRFPPTVFRKHKYLTAFYIVECIAMNSMINTLCFTTV 345  
 Db 270 LVCVVVFAVSWLPLHAFQALAVDIDSOV-LDLKEYKLIFTVFHIIAMCSTFANPLLIGWM 328

QY 346 KNDTVKYF 353  
Db 329 NSNYRKAF 336

## RESULT 8

US-09-200-673-16

; Sequence 16, Application US/09200673A

; Patent No. 6316203

; GENERAL INFORMATION:

; APPLICANT: Gerald, Christophe P.G.

; APPLICANT: Weinschank, Richard L.

; APPLICANT: Walker, Mary W.

; APPLICANT: Branchek, Theresa

; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful

; TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic

; FILE REFERENCE: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)

; CURRENT FILING DATE: 1998-11-25

; EARLIER APPLICATION NUMBER: US/09/200,673A

; EARLIER FILING DATE: 1995-12-01

; EARLIER APPLICATION NUMBER: 08/566,096

; EARLIER FILING DATE: 1994-12-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 381

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-200-673-16

## Query Match

Best Local Similarity 18.9%; Score 387.5; DB 4; Length 381;

Matches: 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;

QY 47 DEDEDVNSRTFFAAKIVIGMALVGVGIGNFTFIAALVRYKKRLNLTLLIANLAI 106

Db 35 DPEPLIDSTKLEIVQVLLAYCISIIILGVIGNSLVHVIKFSKMRVTNFFIANLAV 94

QY 107 SDFLVAIVCCPFENDYVVRQLSWEHGHVCTSVNYLRTVSLVSNALLATAIDRYLAI 166

Db 95 ADLLVNTLCPLFTTYTLAGE--WKMGVPLCHLVPAQGLAVQVSTITLTVIALDRHRCI 152

QY 167 VHLPRMKCOTATGLIALVWTVSIIILAIIPSAFTTETVLVIVKSOEKIFCGOIMPVDOQ 226

Db 153 VYHLESKISKRIISLIIGLAWGISALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEEK 212

QY 227 -LYKSYFLIFGIEFVGPVVTWTLCVARISRELWFKAVPGFQTEIQRKLCRRKTVLV 285

Db 213 SIYGTVYSLSLILYVPLGIISFYSTRWSKLNHVSPGAANDHYHOR--RQKTTKM 269

QY 286 LMCILTAYVLCWAPFYGFTIVRDFPFTVFKYKHLYTAFYIVECIAMNSMINTLCFVTV 345

Db 270 LVCVVVFAVSWLPLHAFQLAVDIDSQV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWM 328

QY 346 KNDTVKYF 353

Db 329 NSNYRKAF 336

## RESULT 9

US-09-407-367-2

; Sequence 2, Application US/09407367

; Patent No. 6420532

; GENERAL INFORMATION:

; APPLICANT: Christophe P.G. Gerald, et al.

; TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper &amp; Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/407,367  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-407-367-2

## Query Match

Best Local Similarity 18.9%; Score 387.5; DB 4; Length 381;

Matches: 91; Conservative 73; Mismatches 137; Indels 7; Gaps 4;

QY 47 DEDEDVNSRTFFAAKIVIGMALVGVGIGNFTFIAALVRYKKRLNLTLLIANLAI 106

Db 35 DPEPLIDSTKLEIVQVLLAYCISIIILGVIGNSLVHVIKFSKMRVTNFFIANLAV 94

QY 107 SDFLVAIVCCPFENDYVVRQLSWEHGHVCTSVNYLRTVSLVSNALLATAIDRYLAI 166

Db 95 ADLLVNTLCPLFTTYTLAGE--WKMGVPLCHLVPAQGLAVQVSTITLTVIALDRHRCI 152

QY 167 VHLPRMKCOTATGLIALVWTVSIIILAIIPSAFTTETVLVIVKSOEKIFCGOIMPVDOQ 226

Db 153 VYHLESKISKRIISLIIGLAWGISALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEEK 212

QY 227 -LYKSYFLIFGIEFVGPVVTWTLCVARISRELWFKAVPGFQTEIQRKLCRRKTVLV 285

Db 213 SIYGTVYSLSLILYVPLGIISFYSTRWSKLNHVSPGAANDHYHOR--RQKTTKM 269

QY 286 LMCILTAYVLCWAPFYGFTIVRDFPFTVFKYKHLYTAFYIVECIAMNSMINTLCFVTV 345

Db 270 LVCVVVFAVSWLPLHAFQLAVDIDSQV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWM 328

QY 346 KNDTVKYF 353

Db 329 NSNYRKAF 336

## RESULT 10

US-08-876-798A-2

; Sequence 2, Application US/08876798A

; Patent No. 6355478

; GENERAL INFORMATION:

; APPLICANT: Baez, Melvyn

; APPLICANT: Yang, Peiyi

; TITLE OF INVENTION: RHESUS MONKEY NEUROPEPTIDE Y RECEPTOR

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company

; STREET: Lilly Corporate Center

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: U.S.A.

; ZIP: 46285

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,798A
; FILING DATE: 16-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)276-0756
; TELEFAX: (317)276-2763
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-876-798A-2

Query Match      18.7%; Score 384.5; DB 4; Length 381;
Best Local Similarity 29.2%; Pred. No. 2.2e-30;
Matches 90; Conservative 74; Mismatches 137; Indels 7; Gaps 4;

QY 47 DEDEDVTSRTFFAAKIVIGMALVGMVLCVGGIGNFIFIAALVRYKKLRNLNLIANLAI 106
Db 35 DPPELIDSTKLEVOVILAYCSILLGVNLSLVHVIKFKSMRTVNFNLANLAV 94

QY 107 SDFLNAIVCCPFEMDYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 166
Db 95 ADLVVNTLCPLFTLTLMGE--WKMGPVLCVLAQGLAVQVSTITLTVALDRHRCI 152

QY 167 VHPLRPMKCATGIALVMTVSVILAIPTSAFTETVTVLVKSOEIKFCQIWPVDOQ 226
Db 153 VYLESKIKRISFLIIGLAWISALASPLAIFREYSLEIIPDFEIVACTERWPGEEK 212

QY 227 -LYKSYFLIFGIEFVGVVVTMTLCYARISRELWFKAVPGFQTEQIRKLRCKRKIVLV 285
Db 213 SIYGTVYSLSLILVLPGLIISFYSYTRISWKLKSHVSPGAANDHYHQ--RQKTKM 269

QY 286 LMCILLAYVLCNAPFGFTIVRDFTPTVVKKHLYTAFYIVECIAMSNSINTLCFTV 345
Db 270 LVCVVYVFAVSLPLHAFQLAVDIDSHV-LDLKEYKLFTVPHIIMCGSTFANPLLYGM 328

QY 346 KNDTVKYF 353
Db 329 NSNYKRAF 336

```

```

RESULT 11
US-08-513-974B-26
; Sequence 26, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-513-974B-26

```

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Query Match      18.0%; Score 370; DB 3; Length 370;
Best Local Similarity 28.5%; Pred. No. 6e-29;
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;

QY 21 SVLNPHGATSPFENFSYSDYDMDPDEDEVTNSRTFFAAKIVIGM--ALVGINLVCG- 77
Db 21 AVTTPANQSAEASAGNSVAGADAPA-----VTPQSLQVLHQLKGLVILVYVVVVGL 75

QY 78 IGNFIFIAALVRYKKLRNLNLIANLAIISDFLVAIVCCPFEMDYVYVYVYVYVYVYV 137
Db 76 VGNCLLVLIARVRLHNVNFIIGNLALSDVLMCTACVPLTL-AYAFEPGRGWFGGLC 134

QY 138 TSVNYLRTVSLVSTNALLAIAIDRYLAIVHPLRPMKCATGIALVMTVSVILAIPTSA 197
Db 135 HLVFPLQPVTVVSVFTLTITIAVDRIYVVLVHPLRRLRRISRLISAYAVLAIALSAVLA 194

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QY 198 AVTTETVLIVKRSQEKIFCGQIWPVDQ---QLYKSYFLFIFGIEFVGPVVTMLCYAR 254  
Db 195 A---VHTYHVELKPHDVRICEEFWGSQEROLYANGLL---VTYLLPLLVILLSYVR 247  
QY 255 ISRELWFKAVPGFQTEIRKRLRC-RRKTVLVLMCILTAYVLCWAPFYGFTIVRDFEFTV 313  
Db 248 VSVKLRNRVPGCVTQSQADWDARRRTFCLLVVVVFAVCWMLPLHVFNLRLDLP-- 305  
QY 314 FVKEKHYLT--AFYIVE--C--IAMSNSMINTLCFTVVKNDTVYFKKIMLLHW 361  
Db 306 -----HAIDPYAFGLVOLLCHLWAMSSACYNPFYAWL-HDSFREELRKLVAW 353

## RESULT 12

US-08-513-974B-323  
; Sequence 323, Application US/08513974B  
; Patent No. 6114139  
; GENERAL INFORMATION:  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Hosoya, Masaki  
; APPLICANT: Fujii, Ryo  
; APPLICANT: Ohtaki, Tetsuya  
; APPLICANT: Fukusumi, Shoji  
; APPLICANT: Ohgi, Kazuhiro  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
; NUMBER OF SEQUENCES: 380  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-007177  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-326611  
; FILING DATE: 28-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-270017  
; FILING DATE: 02-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236357  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236356  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189274  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189273

; FILING DATE: 11-AUG-1945  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 45753  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 323:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 370 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-513-974B-323

Query Match 18.0%; Score 370; DB 3; Length 370;  
Best Local Similarity 28.5%; Pred. No. 6e-29;  
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;  
QY 21 SVLNPHGAHATSPFPNFSYSDYDMPLEDEDEVTNRTFFFAKIVIGM--ALVGMILVCG- 77  
Db 21 AVTTPANGSAEASAGNSVAGADAPA-----VTPFQSLQLVHQLKGLIVLLYSVVVVGL 75  
QY 78 IGNEFTIAALVRYKKRLNLTLLIANLAISDFLVAIVCCPFEMDYVVVRLSWEHGVL 137  
Db 76 VGNCLLVLIARVRRLHNTVFLIGNLALSVDLMCTACVPLTL-AYAFEPGWVFGGGLC 134  
QY 138 TSVNYLRTVSLVSTNALLAIDRYLAIVHPLRPMKQCTATGLIALVMTVSLIAIPS 197  
Db 135 HLVTFLQPTVTVSVETLTTIADVRYVYVHPLRRISRLSAYAVLAIWALSALPALPA 194  
QY 198 AYTETVLIVKRSQEKIFCGQIWPVDQ---QLYKSYFLFIFGIEFVGPVVTMLCYAR 254  
Db 195 A---VHTYHVELKPHDVRICEEFWGSQEROLYANGLL---VTYLLPLLVILLSYVR 247  
QY 255 ISRELWFKAVPGFQTEIRKRLRC-RRKTVLVLMCILTAYVLCWAPFYGFTIVRDFEFTV 313  
Db 248 VSVKLRNRVPGCVTQSQADWDARRRTFCLLVVVVFAVCWMLPLHVFNLRLDLP-- 305  
QY 314 FVKEKHYLT--AFYIVE--C--IAMSNSMINTLCFTVVKNDTVYFKKIMLLHW 361  
Db 306 -----HAIDPYAFGLVOLLCHLWAMSSACYNPFYAWL-HDSFREELRKLVAW 353

## RESULT 13

US-09-172-353-5  
; Sequence 5, Application US/09172353  
; Patent No. 6197530  
; GENERAL INFORMATION:  
; APPLICANT: Stricker-Kongra, Alain  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS  
; FILE REFERENCE: 07334/102001  
; CURRENT APPLICATION NUMBER: US/09/172,353  
; CURRENT FILING DATE: 1998-10-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-172-353-5

Query Match 18.0%; Score 370; DB 3; Length 370;  
Best Local Similarity 28.5%; Pred. No. 6e-29;  
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;  
QY 21 SVLNPHGAHATSPFPNFSYSDYDMPLEDEDEVTNRTFFFAKIVIGM--ALVGMILVCG- 77

Db 21 AVTTPANQSAEASAGNSVAGADAPA-----VTPQSLQVHQLKGLLVLLSVVVVGL 75  
QY 78 IGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVYVQRLSWHGRVLC 137  
Db 76 VGNCLLVLIARVRRLLHNTVFNGLNALSVDLMCTACVPLTL-AYAFEPGRGWVFGGLC 134  
QY 138 TSVNYLRTVSLVSYNALLAIAIDRYLAIVHPLPRMKCQTATGLIALVWTVSILIAIPS 197  
Db 135 HLVEFLQPVTVVSVFTLTIAVDYVVLVHPLRRISRLSAYAVLAWLSAVLALPA 194  
QY 198 AYFTTETVLVIVKSEKIFCGQIWPVQ---OLYKSYFLFIFGIEFGVGPVVTMTLCYAR 254  
Db 195 A---VHTYHVELKPHDVRCLCEEFWGSQERQOLYAWGLL---VTYLLPLLVILLSYVR 247  
QY 255 ISRELWFAVPGFQTEQIRKRLC-RRKTVLVLMCLITAYVLCWAPFGFTIVRDFPTV 313  
Db 248 VSVKLRNVPCVQTSQADMDRARRRRTFCLLVVVVFAVCWMLPLHVFNLRLDLP-- 305  
QY 314 FVKEKHYLT--AFYIVE--C--IAMSNSMINTLCFVTVKNDTVKFKKIMLLRW 361  
Db 306 -----HAIDPYAFLVQLLCHWLANSSACYNFFIYAWL-HDSFREELKLLVAV 353

## RESULT 14

US-08-776-971-21  
; Sequence 21, Application US/08776971B  
; Patent No. 6228984

## GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji  
Habata, Yugo  
Kawamata, Yuji  
Hosoya, Masaki  
Fujii, Ryo  
Fukusumi, Shoji  
Kitada, Chieko  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,971B  
FILING DATE: 06-Feb-1997

## CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/03821  
FILING DATE: 28-DEC-1996  
APPLICATION NUMBER: JP 7/343371  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: JP 8/59419  
FILING DATE: 15-MAR-1996  
APPLICATION NUMBER: JP 8/211805  
FILING DATE: 12-AUG-1996  
APPLICATION NUMBER: JP 8/246573  
FILING DATE: 18-SEP-1996

## ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.  
REGISTRATION NUMBER: 27,026  
REFERENCE/DOCKET NUMBER: 47176  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:

LENGTH: 370 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-08-776-971-21

Query Match 18.0%; Score 370; DB 3; Length 370;  
Best Local Similarity 28.5%; Pred. No. 6e-29;  
Matches 101; Conservative 75; Mismatches 144; Indels 34; Gaps 13;

QY 21 SVLNPHGAAATSEFFNFESYSDYDMPDDEDEDVTSRTFAAKIVIGM-ALVGIMLVCG- 77  
Db 21 AVTTPANQSAEASAGNSVAGADAPA-----VTPQSLQVHQLKGLLVLLSVVVVGL 75  
QY 78 IGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEMDYVYVYVQRLSWHGRVLC 137  
Db 76 VGNCLLVLIARVRRLLHNTVFNGLNALSVDLMCTACVPLTL-AYAFEPGRGWVFGGLC 134  
QY 138 TSVNYLRTVSLVSYNALLAIAIDRYLAIVHPLPRMKCQTATGLIALVWTVSILIAIPS 197  
Db 135 HLVEFLQPVTVVSVFTLTIAVDYVVLVHPLRRISRLSAYAVLAWLSAVLALPA 194  
QY 198 AYFTTETVLVIVKSEKIFCGQIWPVQ---OLYKSYFLFIFGIEFGVGPVVTMTLCYAR 254  
Db 195 A---VHTYHVELKPHDVRCLCEEFWGSQERQOLYAWGLL---VTYLLPLLVILLSYVR 247  
QY 255 ISRELWFAVPGFQTEQIRKRLC-RRKTVLVLMCLITAYVLCWAPFGFTIVRDFPTV 313  
Db 248 VSVKLRNVPCVQTSQADMDRARRRRTFCLLVVVVFAVCWMLPLHVFNLRLDLP-- 305  
QY 314 FVKEKHYLT--AFYIVE--C--IAMSNSMINTLCFVTVKNDTVKFKKIMLLRW 361  
Db 306 -----HAIDPYAFLVQLLCHWLANSSACYNFFIYAWL-HDSFREELKLLVAV 353

## RESULT 15

US-08-776-971-104  
; Sequence 104, Application US/08776971B  
; Patent No. 6228984

## GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji  
Habata, Yugo  
Kawamata, Yuji  
Hosoya, Masaki  
Fujii, Ryo  
Fukusumi, Shoji  
Kitada, Chieko  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

Search completed: October 7, 2003, 09:53:26  
Job time : 22 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:50:12 ; Search time 39 Seconds

(without alignments)  
2600.376 Million cell updates/sec

Title: US-10-070-240A-1

Perfect score: 2055

Sequence: 1 MWTMGPMDDNAINSTSF.....LDLKTIGMPATEEVDICRLK 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriaph:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID        | Description         |
|------------|--------|-------------|--------|-----------|---------------------|
| 1          | 2055   | 100.0       | 393    | 4 Q8TCW9  | Q8TCW9 homo sapien  |
| 2          | 2049   | 99.7        | 393    | 4 Q8NFJ7  | Q8NFJ7 homo sapien  |
| 3          | 1915   | 93.2        | 393    | 6 Q8SPN2  | Q8SPN2 bos taurus   |
| 4          | 1767   | 86.0        | 393    | 11 Q8R416 | Q8R416 rattus norv  |
| 5          | 1766   | 85.9        | 384    | 4 Q8NFJ6  | Q8NFJ6 homo sapien  |
| 6          | 1764   | 85.8        | 393    | 11 Q9JKL1 | Q9JKL1 mus musculus |
| 7          | 1719   | 83.6        | 384    | 6 Q8SPN1  | Q8SPN1 bos taurus   |
| 8          | 1715.5 | 83.5        | 421    | 11 Q8R415 | Q8R415 rattus norv  |
| 9          | 1703   | 82.9        | 355    | 4 Q9NTT0  | Q9NTT0 homo sapien  |
| 10         | 1699.5 | 82.7        | 381    | 11 Q8K458 | Q8K458 mus musculus |
| 11         | 1020   | 49.6        | 220    | 11 Q8BIR4 | Q8BIR4 mus musculus |
| 12         | 407    | 19.8        | 449    | 5 Q9VB87  | Q9VB87 drosophila   |
| 13         | 401.5  | 19.5        | 381    | 11 Q9ERC0 | Q9ERC0 rattus norv  |
| 14         | 401    | 19.5        | 465    | 5 Q44Z26  | Q44Z26 lymanaea sta |
| 15         | 399.5  | 19.4        | 678    | 5 Q94736  | Q94736 stomoxys ca  |
| 16         | 389.5  | 19.0        | 381    | 11 Q8BWL1 | Q8BWL1 mus musculus |

|    |       |      |     |           |                     |
|----|-------|------|-----|-----------|---------------------|
| 17 | 382.5 | 18.6 | 519 | 5 Q9VAD2  | Q9VAD2 drosophila   |
| 18 | 377.5 | 18.4 | 517 | 5 Q8TOS8  | Q8TOS8 drosophila   |
| 19 | 367   | 17.9 | 504 | 5 Q9VX8   | Q9VX8 drosophila    |
| 20 | 360.5 | 17.5 | 407 | 11 Q8BIR7 | Q8BIR7 mus musculus |
| 21 | 360   | 17.5 | 384 | 11 Q8BZV9 | Q8BZV9 mus musculus |
| 22 | 357.5 | 17.4 | 431 | 5 Q8TBD1  | Q8TBD1 urechis uni  |
| 23 | 356   | 17.3 | 398 | 4 Q9UDE6  | Q9UDE6 homo sapien  |
| 24 | 355.5 | 17.3 | 370 | 13 Q8UWL5 | Q8UWL5 fugu rubrip  |
| 25 | 354.5 | 17.3 | 311 | 11 Q8RLR6 | Q8RLR6 cavia porce  |
| 26 | 351   | 17.1 | 398 | 4 Q8NGQ8  | Q8NGQ8 homo sapien  |
| 27 | 351   | 17.1 | 425 | 4 Q9HBV6  | Q9HBV6 homo sapien  |
| 28 | 344   | 16.7 | 364 | 11 Q8BV78 | Q8BV78 mus musculus |
| 29 | 344   | 16.7 | 460 | 11 Q8BG12 | Q8BG12 mus musculus |
| 30 | 341   | 16.6 | 427 | 5 Q9N324  | Q9N324 caenorhabdi  |
| 31 | 340.5 | 16.6 | 600 | 5 Q9VW75  | Q9VW75 drosophila   |
| 32 | 339.5 | 16.5 | 367 | 13 Q9PVG0 | Q9PVG0 carassius a  |
| 33 | 339   | 16.5 | 411 | 13 Q9M613 | Q9M613 gallus gall  |
| 34 | 338   | 16.4 | 429 | 5 P92045  | P92045 lymanaea sta |
| 35 | 337.5 | 16.4 | 367 | 13 Q9PVF9 | Q9PVF9 carassius a  |
| 36 | 337   | 16.4 | 380 | 13 Q9DGQ6 | Q9DGQ6 carassius a  |
| 37 | 335   | 16.3 | 390 | 13 Q8JFP8 | Q8JFP8 bufo marinu  |
| 38 | 333.5 | 16.2 | 377 | 13 Q8QGM3 | Q8QGM3 gallus gall  |
| 39 | 332.5 | 16.2 | 402 | 5 Q964E5  | Q964E5 dugesia tig  |
| 40 | 332.5 | 16.2 | 450 | 5 Q8T5J7  | Q8T5J7 anopheles g  |
| 41 | 332   | 16.2 | 309 | 13 Q9DGJ9 | Q9DGJ9 bufo marinu  |
| 42 | 329   | 16.0 | 385 | 11 Q8BQ97 | Q8BQ97 mus musculus |
| 43 | 327   | 15.9 | 452 | 11 Q9JKN0 | Q9JKN0 mus musculus |
| 44 | 326.5 | 15.9 | 346 | 6 Q95KS6  | Q95KS6 oviv aries   |
| 45 | 323   | 15.7 | 422 | 11 Q8VHD7 | Q8VHD7 rattus norv  |

## ALIGNMENTS

RESULT 1

| ID | Q8TCW9  | PRELIMINARY; | PRT; | 393 AA. |
|----|---|--------------|------|---------|
| AC | Q8TCW9;   |              |      |         |
| DT | 01-JUN-2002 (TREMUREL. 21, Created)   |              |      |         |
| DT | 01-JUN-2002 (TREMUREL. 21, Last sequence update)  |              |      |         |
| DT | 01-MAR-2003 (TREMUREL. 23, Last annotation update)  |              |      |         |
| DE | G protein-coupled receptor ZAG (GPR73).   |              |      |         |
| GN | GPR73.  |              |      |         |
| OS | Homo sapiens (Human).   |              |      |         |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;   |              |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.   |              |      |         |
| OX | NCBI_TaxID=9606;  |              |      |         |
| RN | [1]   |              |      |         |
| RP | SEQUENCE FROM N.A.  |              |      |         |
| RA | Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;  |              |      |         |
| RT | *Purification and identification of EG-VEGF family as cognate ligands for two orphan G protein-coupled receptors.*; |              |      |         |
| RL | Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.   |              |      |         |
| RN | [2]   |              |      |         |
| RP | SEQUENCE FROM N.A.  |              |      |         |
| EX | MEDLINE-22314729; PubMed-12427552;  |              |      |         |
| RA | Soga T., Matsumoto S., Oda T., Saito T., Hiyama H., Takasaki J.,  |              |      |         |
| RA | Kamohara M., Ohishi T., Matsushime H., Furuichi K.;   |              |      |         |
| RT | *Molecular cloning and characterization of prokineticin receptors.*;  |              |      |         |
| RL | Biochim. Biophys. Acta 1579:173-179(2002).  |              |      |         |
| DR | EMBL; AY089976; AAM11892.1; -   |              |      |         |
| DR | EMBL; AB084080; BAC24021.1; -   |              |      |         |
| DR | Interpro; IPR000276; GPCR_Rhodopsin.  |              |      |         |
| DR | Pfam; PF00001; 7tm_1; 1.  |              |      |         |
| DR | PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.  |              |      |         |
| DR | PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.  |              |      |         |
| KW | Receptor.   |              |      |         |
| SQ | SEQUENCE 393 AA; 44769 MW; OD36461CA99CAZC1 CRC64;  |              |      |         |

Query Match 100.0%; Score 2055; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.2e-183;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTTMGFMDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDDEDEDVNSRTFFA 60
DB 1 MTTMGFMDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDDEDEDVNSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
DB 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVLMCILTAIVLWCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVLMCILTAIVLWCWAPF 300
QY 301 YGFTIVRDFPPTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDFPPTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICIRLK 393
DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICIRLK 393
RESULT 2
QY Q8NFJ7 PRELIMINARY; PRT; 393 AA.
AC Q8NFJ7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Prokineticin receptor 1.
GN PKRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22028034; PubMed=11886876;
RA Lin D.C.H., Bullock C.M., Ehler F.J., Chen J.L., Tian H., Zhou Q.Y.;
RT Identification and Molecular Characterization of Two Closely Related
RT G Protein-coupled Receptors Activated by Prokineticins/Endocrine Gland
RT Vascular Endothelial Growth Factor.*;
RL J. Biol. Chem. 277:19276-19280(2002).
DR EMBL; AF506287; AAM48127.1; -.
DR Genbank; HGNC:4524; GPR73.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; 1.
DR PROSITE; PS02062; G_PROTEIN_RECEPTOR_FL2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44802 MW; AA085F33B789AEC7 CRC64;
Query Match 99.7%; Score 2049; DB 4; Length 393;
Best Local Similarity 99.5%; Pred. No. 4.2e-183;
Matches 391; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTTMGFMDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDDEDEDVNSRTFFA 60
DB 1 MTTMGFMDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDDEDEDVNSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
DB 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
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DB 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVLMCILTAIVLWCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVLMCILTAIVLWCWAPF 300
QY 301 YGFTIVRDFPPTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDFPPTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
QY 361 WKASYNGKSSADLDLKTIGMPATEEVDICIRLK 393
DB 361 WKASYNGKSSADLDLKTIGMPATEEVDICIRLK 393
RESULT 3
QY Q8SPN2 PRELIMINARY; PRT; 393 AA.
AC Q8SPN2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE G protein-coupled receptor 2A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
RT Purification and identification of EG-VGFP family as cognate ligands
RT for two orphan G protein-coupled receptors.*;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY089972; AAM11888.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; 1.
DR PROSITE; PS02062; G_PROTEIN_RECEPTOR_FL2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44602 MW; CF302DD364D8A2CC CRC64;
Query Match 93.2%; Score 1915; DB 6; Length 393;
Best Local Similarity 92.4%; Pred. No. 1.4e-170;
Matches 363; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
QY 1 MTTMGFMDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDDEDEDVNSRTFFA 60
DB 1 MTTMGFMDNATNTSTFSLVNLPHGAHATSPFNFSYSDYDMPDDEDEDVNSRTFFA 60
QY 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
DB 61 AKIVIGMALVGLVCGIGNFIFIAALVRYKKLRNLNLLIANLAISDFLVAIVCCPFEM 120
QY 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
DB 121 DYVVRQLSWEHGHVLTCTSVNLTSLVSTNALLAIAIDRYLAIVHPLRPRMKCQTAT 180
QY 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
DB 181 GLIALVMTVSLIIAIPSAFYTTETVLVIVKSOEKIFCGQIWPVDOQLYKSYFLFIFGIE 240
QY 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVLMCILTAIVLWCWAPF 300
DB 241 FVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRKRKTVLVLMCILTAIVLWCWAPF 300
QY 301 YGFTIVRDFPPTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
DB 301 YGFTIVRDFPPTVFKKHYLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIMLLH 360
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Db 301 YGFAIVRDFEFTVFVKERHYLTAFAVVECIAMNSMINTVCFVTYKNTIKYFKKIMLLH 360
QY 361 WKASYNGKSSADLDLKTIGMPATEVDCIRLK 393
Db 361 WKASYNGKSSGDLKLTGTGVPATEVDCIGLK 393

RESULT 4
Q8R416 PRELIMINARY: PRT: 393 AA.
AC Q8R416;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE G protein-coupled receptor ZAQ.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;
RT "Purification and identification of EG-VGFR family as cognate ligands
for two orphan G protein-coupled receptors."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY085974; AAM11890.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 44507 MW; C75EC72B97E503A8 CRC64;

Query Match 86.0%; Score 1767; DB 11; Length 393;
Best Local Similarity 84.0%; Pred. No. 9.4e-157;
Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 MTTMGFDNDNATNSTSLVSNPHGAHATSFNFYSYDMDPLDEEDVNSRTFFA 60
Db 1 MTTVTGIGENTNTFTDFSSARDGSAETSPLPTFSYGDYDMPDSEEDVNSRTFFA 60

QY 61 AKIVIGMALVGLMVCIGGNFTIFIAALVRYKKRLNLTNLIANLAISDFLVAIVCCPFEM 120
Db 61 AKIVIGMALVGLMVCIGGNFTIFIALARYKKRLNLTNLIANLAISDFLVAIVCCPFEM 120

QY 121 DYVVYRQLSWEGHGVLCISVNYLRTVSVLSTNALLAIDAIDRYLAIVHPLRPMKCQTAT 180
Db 121 DYVVYRQLSWEGHGVLCASVNYLRTVSVLSTNALLAIDAIDRYLAIVHPLRPMKCQTAA 180

QY 181 GLIALVMTYSILIAIPSAFTTETVLVIVKSEKIFCGQIWPVDOOLYKSYFLFIFGIE 240
Db 181 GLIFLWMSYILIAIPAAFTTETVLVIVSEKIFCGQIWPVDOQFYYSYFLVFLGLE 240

QY 241 FYGVPVMTLCVARSRELWFAVPGFQTEQIRKRLCRKRVLVLMCLITAYVLCWAPF 300
Db 241 FYGVPVMTLCVARSRELWFAVPGFQTEQIRKRLCRKRVLVGLCVLSAYVLCWAPF 300

QY 301 YGFTIVRDFEFTVFVKERHYLTAFAVVECIAMNSMINTLCFVTYKNDTVKYFKKIMLLH 360
Db 301 YGFTIVRDFEFTVFVKERHYLTAFAVVECIAMNSMINTLCFVTYKNTIKYFKKIMLLH 360

QY 361 WKASYNGKSSADLDLKTIGMPATEVDCIRLK 393
Db 361 WRASPSGSKASADLDLKTIGMPATEVDCIRLK 393

RESULT 5
Q8NFJ6 PRELIMINARY: PRT: 384 AA.
AC Q8NFJ6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
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DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Prokineticin receptor 2 (GPRG2).
GN PXR2 OR GPRG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin D.C.H., Bullock C.M., Ehler F.J., Chen J.L., Tian H., Zhou Q.Y.;
RT "Identification and Molecular Characterization of Two Closely Related
G Protein-coupled Receptors Activated by Prokineticins/Endocrine Gland
Vascular Endothelial Growth Factor."
RL J. Biol. Chem. 277:19276-19280(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=22314729; PubMed=11886876;
RA Lin D.C.H., Bullock C.M., Ehler F.J., Chen J.L., Tian H., Zhou Q.Y.;
RT "Identification and Molecular Characterization of Two Closely Related
G Protein-coupled Receptors Activated by Prokineticins/Endocrine Gland
Vascular Endothelial Growth Factor."
RL J. Biol. Chem. 277:19276-19280(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=22314729; PubMed=12427552;
RA Soga T., Matsumoto S., Oda T., Saito T., Miyama H., Takasaki J.,
RA Kamohara M., Ohishi T., Matsushime H., Furuichi K.;
RT "Molecular cloning and characterization of prokineticin receptors."
RL Biochim. Biophys. Acta 1579:173-179(2002).
DR EMBL: AF506288; AAM48128.1; -.
DR EMBL: AB084081; BAC24022.1; -.
DR Genew; HGNC:15836; GPR73L1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 384 AA; 43995 MW; 2D5BFA3655347B5E CRC64;

Query Match 85.9%; Score 1766; DB 4; Length 384;
Best Local Similarity 87.4%; Pred. No. 1.1e-156;
Matches 334; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 12 ATNTSTSLVSNPHGAHATSFNFYSYDMDPLDEEDVNSRTFFAIVIGMALVG 71
Db 3 AONGTSETPNFNPQDHASLSFNSYGDYDLPDEEDVNSRTFFAIVIGMALG 62

QY 72 IMLVCGIGNFTIFIAALVRYKKRLNLTNLIANLAISDFLVAIVCCPFEMDYVVYRQLSWE 131
Db 63 IMLVCGIGNFTIFIAALTRYKKRLNLTNLIANLAISDFLVAIVCCPFEMDYVVYRQLSWE 122

QY 132 HGVLCISVNYLRTVSVLSTNALLAIDAIDRYLAIVHPLRPMKCQTATGLIALVMTVSI 191
Db 123 HGVLCASVNYLRTVSVLSTNALLAIDAIDRYLAIVHPLRPMKYQTASFIALVMTVSI 182

QY 192 LIAIPSAFTTETVLVIVKSEKIFCGQIWPVDOOLYKSYFLFIFGIEFYGVVMTLC 251
Db 183 LIAIPSAFATETVLVIVKSEKIFCGQIWPVDOOLYKSYFLFIFGIEFYGVVMTLC 242

QY 252 YARISRELWFAVPGFQTEQIRKRLCRKRVLVLMCLITAYVLCWAPFYGTIVRDFE 311
Db 243 YARISRELWFAVPGFQTEQIRKRLCRKRVLVLMCLITAYVLCWAPFYGTIVRDFE 302

QY 312 TVFYKERYLTAFAVVECIAMNSMINTLCFVTYKNDTVKYFKKIMLLHNSKASNGKSS 371
Db 303 TVFYKERYLTAFAVVECIAMNSMINTVCFVTYKNTIKYFKKIMLLHWPSPGSKSS 362

QY 372 ADLDLKTIGMPATEVDCIRLK 393
Db 363 ADLDLRTNGVPTTEVDCIRLK 384

RESULT 6
Q9JKL1 PRELIMINARY: PRT: 393 AA.
ID Q9JKL1;
AC Q9JKL1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
```

DE G-protein coupled receptor GPR73 (Prokineticin receptor 1).  
 GN GPR73 OR PKRI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20225484; PubMed=10760605;  
 RA Parker R., Liu M., Eyre H.J., Copeland N.G., Gilbert D.J.,  
 Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;  
 RT "Y-receptor-like genes GPR72 and GPR73: molecular cloning, genomic  
 organisation and assignment to human chromosome 11q21.1 and 2p14 and  
 mouse chromosome 9 and 6";  
 RL Biochim. Biophys. Acta 1491:369-375(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6;  
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,  
 Weaver D.R., Leslie F.M., Zhou O.Y.;  
 RT "Prokineticin 2 transmits the behavioural circadian rhythm of the  
 suprachiasmatic nucleus";  
 RL Nature 417:405-410(2002).  
 DR EMBL: AF236082; AAF43706.1; -;  
 DR EMBL: AF487278; AAM49570.1; -;  
 DR MGD: MGI:1929676; Gpr73.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 393 AA: 44528 MW: 46F5E78C00DC871C CRC64;

Query Match 85.8%; Score 1764; DB 11; Length 393;  
 Best Local Similarity 84.0%; Pred. No. 1.8e-156;  
 Matches 330; Conservative 30; Mismatches 33; Indels 0; Gaps 0;  
 QY 1 METTGFMDDNATNTSTFLSVLNPNGAHATSPFNFSYSDYDMLDEDEDVTSRTFFA 60  
 DB 1 METTVGALCENTDTFTDFFSALDQHEAQTSGLPFTFSYGDYDMLDEDEDVTSRTFFA 60  
 QY 61 AKIVIGMALGVMLVCGIGNFTFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPEM 120  
 DB 61 AKIVIGMALGVMLVCGIGNFTFIALARYKKLRNLTNLLIANLAISDFLVAIVCCPEM 120  
 QY 121 DYVVYRQLSWERGHVLCSTVNYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMKCQTAT 180  
 DB 121 DYVVYRQLSWERGHVLCASVNYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMKCQTAA 180  
 QY 181 GLIALWTVSYLIIATPSAYFTTETVLVIVKSEKIFCGIWPVDOOLYKSYFLFIRGIE 240  
 DB 181 GLIFLWMSVSIILAIAPAAFTTETVLVIVEROEKIFCGIWPVDOOFYRYSFLFVFGLE 240  
 QY 241 FVGPPVMTLCLYARISRELWFKAVPGFQTEQIRKLRRCRRKTVLVMCLITAYVLCNAPF 300  
 DB 241 FVGPPVMTLCLYARISRELWFKAVPGFQTEQIRRVRCRRRTVLGLVCLVSLAYVLCNAPF 300  
 QY 301 YGTTIVRDFPFPVVKKEHYLTAIFYVECIAMNSMINTLCFTVVKNDTVYFKKIMLLH 360  
 DB 301 YGTTIVRDFPFPVVKKEHYLTAIFYVECIAMNSMINTLCFTVVRNNTSKYLARILQ 360  
 QY 361 WKASVNGKSSADLDLTKTGMPATEEVDICRLK 393  
 DB 361 WRASPSGSKASADLDLRTTGIPATEEVDICRLK 393

RESULT 7  
 Q8SPN1 PRELIMINARY; PRT; 384 AA.  
 AC Q8SPN1;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE G protein-coupled receptor 15E.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;  
 RT "Purification and identification of EG-VeGF family as cognate ligands  
 for two orphan G protein-coupled receptors.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AV089973; AAM11889.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 384 AA: 44138 MW: 997895960EEB2DD4 CRC64;  
 Query Match 83.6%; Score 1719; DB 6; Length 384;  
 Best Local Similarity 84.3%; Pred. No. 2.8e-152;  
 Matches 322; Conservative 29; Mismatches 31; Indels 0; Gaps 0;  
 QY 12 ATNTSTFLSVLNPNGAHATSPFNFSYSDYDMLDEDEDVTSRTFFAIVIGMALVG 71  
 DB 3 AQGNASPPANFSIPOEHASSUPFNFSYDYLDEDEDMTKTOTFAAKIVIGVALVG 62  
 QY 72 IMLVCGIGNFTFIAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPEMDYVYVRLSWE 131  
 DB 63 IMLTGCIGNFTFIALTRYKKLRNLTNLLIANLAISDFLVAIVCCPEMDYVYVHLSWE 122  
 QY 132 HGVLCSTVNYLRTVSVLSTNALLAIAIDRYLAIVHPLPRMKCQTATGLIALWTVSY 191  
 DB 123 HGVLCACINYLRTVSVLSTNALLAIAIDRYLAIVHPLKPMNYQTASFIALWVYSI 182  
 QY 192 LTAIPSAVYTTETVLVIVKSEKIFCGIWPVDOOLYKSYFLFIFGIEFVGPPVMTLCL 251  
 DB 183 LISIPSAVYTKETVLVIVKSKIFCGIWPVDOOLYKSYFLFIFGIEFVGPPVMTLCL 242  
 QY 252 YARISRELWFKAVPGFQTEQIRKLRRCRRKTVLVMCLITAYVLCNAPFYGTTIVRDFP 311  
 DB 243 YARISRELWFKAVPGFQTEQIRKLRRCRRKTVLVMCLITAYVLCNAPFYGTTIVRDFP 302  
 QY 312 TVFVKEKHLYTAIFYVECIAMNSMINTLCFTVVKNDTVYFKKIMLLHWSYNGSKSS 371  
 DB 303 TVFVKEKHLYTAIFYVECIAMNSMINTVCFVTVKNSTMKYFKKMLLLWRPSSHGSKSS 362  
 QY 372 ADLDAKTGMPATEEVDICRLK 393  
 DB 363 ADLDAKTSRLPATEEVDICRLK 384  
 RESULT 8  
 Q8R415 PRELIMINARY; PRT; 421 AA.  
 AC Q8R415;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE G protein-coupled receptor 15E.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Sprague-Dawley;  
 RA Masuda Y., Takatsu Y., Ohtaki T., Shintani Y., Terao Y.;  
 RT "Purification and identification of EG-VeGF family as cognate ligands  
 for two orphan G protein-coupled receptors.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY089975; AAM11891.1; -  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEPT\_F1\_1; 1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEPT\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 421 AA; 47870 MW; AC98D113D1CG4DC3 CRC64;

Query Match 83.5%; Score 1715.5; DB 11; Length 421;  
Best Local Similarity 85.3%; Pred. No. 6.6e-152;  
Matches 324; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

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QY 14 NTSTFSLVNLPHGAHATSEFPNFSYSDYDMPDDEDEVTNSRTFFAAKIYIGMALVGM 73
DB 43 NGNTSFADLPNPQDQVHVSLLPLNYSYGYDIPDDDDVTKTQTFFAKIYIGVALAGIM 102

QY 74 LVCGIGNFIFIAALVRYKKRLNLTLLIANLAISDFLVAIVCCPFEMDYVYVROLSEHG 133
DB 103 LVCGVGNFVFAALARYKKRLNLTLLIANLAISDFLVAIVCCPFEMDYVYVROLSEHG 162

QY 134 HVLCTSVNLYRTSVLYSTNALLATAIDRYLAIVHPLPRMKQATGLIAVTVSILI 193
DB 163 HVLCAVSNLYRTSVLYSTNALLATAIDRYLAIVHPLX-RMNYQTASFLLIAVVMVSI 221

QY 194 AIPSAFTTETVLVIVKSOEKIFCGIWPVDQLYKSYFLIFGIEFVGPVWTMLCYA 253
DB 222 AIPSAFTTETILVIVKQKRLFCQGIWPVDQLYKSYFLIFVGLFVGPVWTMLCYA 281

QY 254 RISRELMFKAVPGFQTEQIRKRLCRRTVLMCILTAIVLCWAPFYGFTIVRDFFTV 313
DB 282 RISQELMFKAVPGFQTEQIRKRLCRRTVLLMLGILTAYVLCWAPFYGFTIVRDFFTL 341

QY 314 FYKEKHLYTAFVIVCIAMNSMINTLCFTVTKNDTVYFKKIMLLHWKASVNGKSSAD 373
DB 342 VYKEKHLYTAFVIVCIAMNSMINTFCFTVTKNTHYFKKIMLLHWKASVNGKSSAD 401

QY 374 LDLKTIGMPATEEVDICIRLK 393
DB 402 LDLKTSGVPAATEEVDICIRLK 421

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# RESULT 9

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Q9NTT0
ID AC Q9NTT0 PRELIMINARY; PRT; 355 AA.
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE DJ680N4.3 (Novel G-protein coupled receptor similar to mouse GPR73)
DE (Fragment).
GN DJ680N4.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collier R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL121755; CAB89854.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEPT_F1_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 355 AA; 40884 MW; 63F308D775B5B3A6 CRC64;

```

Query Match 82.9%; Score 1703; DB 4; Length 355;  
Best Local Similarity 90.1%; Pred. No. 8e-151;  
Matches 320; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

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QY 39 YSDYDMPDDEDEVTNSRTFFAAKIYIGMALVGMVCGIGNFIFIAALVRYKKRLNLTN 98
DB 1 YGYDLPMDDEDEMTKTRTFFAAKIYIGIALGIMLVCGIGNFVFAALTRYKKRLNLTN 60

QY 99 LLIANLAISDFLVAIVCCPFEMDYVYVROLSEHGVLCTSVNLYRTSVLYSTNALLAI 158
DB 61 LLIANLAISDFLVAIICCPFEMDYVYVROLSEHGVLCAVSNLYRTSVLYSTNALLAI 120

QY 159 AIDRYLAIVHPLPRMKQATGLIAVTVSILIIPSAYFTTETVLVIVKSOEKIFCG 218
DB 121 AIDRYLAIVHPLPRMNYQTASFLLIAVVMVSIIPSAYFATETVFLVIVKSOEKIFCG 180

QY 219 QIWPVDQLYKSYFLIFGIEFVGPVWTMLCYARISRELMFKAVPGFQTEQIRKRLRC 278
DB 181 QIWPVDQLYKSYFLIFGIEFVGPVWTMLCYARISRELMFKAVPGFQTEQIRKRLRC 240

QY 279 RRTKTVLMCILTAIVLCWAPFYGFTIVRDFFTVYFKKHYLTAFVIVCIAMNSMIN 338
DB 241 RRTKTVLMCILTAIVLCWAPFYGFTIVRDFFTVYFKKHYLTAFVIVCIAMNSMIN 300

QY 339 TLFCTVTKNDTVYFKKIMLLHWKASVNGKSSADLDLKTIGMPATEEVDICIRLK 393
DB 301 TVCEVTYKNTTHYFKKIMLLHWKASVNGKSSADLDLRTNGVPTTEEVDICIRLK 355

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# RESULT 10

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Q8K458
ID Q8K458 PRELIMINARY; PRT; 381 AA.
AC Q8K458;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Prokineticin receptor 2 (DJ680N4.3).
GN GPR73L1 OR PRK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22022134; PubMed=12024206;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RL suprachiasmatic nucleus.";
RN Nature 417:405-410(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL: AF487279; AAM49571.1; -
DR EMBL: AK041586; BAC30994.1; -
DR EMBL: AK080980; BAC38103.1; -
DR MGD: MGI:2181363; Gpr73l1.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 381 AA; 43375 MW; 1981FD101324166D CRC64;

```

Query Match 82.7%; Score 1699.5; DB 11; Length 381;  
Best Local Similarity 85.0%; Pred. No. 1.8e-150;  
Matches 323; Conservative 26; Mismatches 28; Indels 3; Gaps 1;

|  |  |   |                           |
|--|--|---|---------------------------|
| Qy   | 14   | NTSTSLFLVNLPHGABATSPFPNFSYSDYDMPDLDEDDVTNSRTFFAAKIVIGMALVGLIM | 73                        |
| Db   | 5  | NRNTSPADLNPPODHYV---LNYSGDYDLPCEDEDVTKTQTFPAKIVIGVALGIM       | 61                        |
| Qy   | 74   | LVCIGINFIFIAALVRYKKLRNLTNLNLIANLAISDFVAIVCCPFEMDYVYVYVQLSWEHG | 133                       |
| Db   | 62   | LVCIGINFVFAALARYKKLRNLTNLNLIANLAISDFVAIVCCPFEMDYVYVYVQLSWAHG  | 121                       |
| Qy   | 134  | HVLCTSVNLRTSVLSYVSTNALLAIAIADRYLAIVHPLRPMKQATATGLIALVYVTSILI  | 193                       |
| Db   | 122  | HVLCAVNLRTSVLSYVSTNALLAIAIDRYLAIVHPLRPMKQATATGLIALVYVTSILI    | 181                       |
| Qy   | 194  | AIPSAFTTETVLVIVKSOEKIFCGIWPVDQQLYKYSYFLFIFGIEFVGVPVVTMTLCYA   | 253                       |
| Db   | 182  | AVPSAYFTTETVLVIVKSOEKIFCGIWPVDQQLYKYSYFLFIFGIEFVGVPVVTMTLCYA  | 241                       |
| Qy   | 254  | RISRELFAKVPGGTQEQIRKRLCRKRTVLVLMCILTAYVLCWAPFYGFTIVRDFPTV     | 313                       |
| Db   | 242  | RISQELFAKVPGGTQEQIRKRLCRKRTVLVLMCILTAYVLCWAPFYGFTIVRDFPTV     | 301                       |
| Qy   | 314  | FVKEKHLYTAFYIVVECIAMNSMINTLCFTVTKNDTVYKFKIMLLHWKASYNGKSSAD    | 373                       |
| Db   | 302  | VYKEKHLYTAFYIVVECIAMNSMINTLCFTVTKNDTVYKFKIMLLHWKASYNGKSSAD    | 361                       |
| Qy   | 374  | LDLKTIGHPATEEVDICIRLK 393                                     |                           |
| Db   | 362  | LDLKTSGVPATEEVDICIRLK 381                                     |                           |
| RESULT 11  |  |   |                           |
| Q8BIR4   | ID   | Q8BIR4  | PRELIMINARY; PRT: 220 AA. |
| AC   | Q8BIR4   |   |                           |
| DT   | 01-MAR-2003  | (TRENBLrel. 23, Created)                                      |                           |
| DT   | 01-MAR-2003  | (TRENBLrel. 23, Last sequence update)                         |                           |
| DT   | 01-MAR-2003  | (TRENBLrel. 23, Last annotation update)                       |                           |
| DE   | DJ680N4.3  |   |                           |
| OS   | Eus musculus (Mouse).  |   |                           |
| OC   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |   |                           |
| OC   | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.     |   |                           |
| OX   | NCBI_TaxID=10090;  |   |                           |
| RN   | [1]  |   |                           |
| RP   | SEQUENCE FROM N.A.   |   |                           |
| RC   | STRAIN=C57BL/6J; TISSUE=Pituitary;                                     |   |                           |
| RA   | MEDLINE=22354683; PubMed=12466851;                                     |   |                           |
| RA   | The FANTOM Consortium,   |   |                           |
| RA   | "Analysis of the mouse transcriptome based on functional annotation of |   |                           |
| RT   | 60,770 full-length cDNAs."   |   |                           |
| RL   | Nature 420:563-573(2002).  |   |                           |
| DR   | EMBL: AK030458; BAC26971.1;  |   |                           |
| SQ   | SEQUENCE 220 AA; 25384 MW; ASE4379BE21109B5 CRC64;                     |   |                           |
| Query Match 49.6%; Score 1020; DB 11; Length 220;              |  |   |                           |
| Best Local Similarity 86.4%; Pred. No. 3e-87;                  |  |   |                           |
| Matches 190; Conservative 18; Mismatches 12; Indels 0; Gaps 0; |  |   |                           |
| Qy   | 174  | MKQTAGLIALVYVTSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQQLYKYSYF      | 233                       |
| Db   | 1  | MYQTAGLIALVYVTSILIAIPSAFTTETVLVIVKSOEKIFCGIWPVDQQLYKYSYF      | 60                        |
| Qy   | 234  | LFIFGIEFVGVPVVTMTLCYARISRELFAKVPGGTQEQIRKRLCRKRTVLVLMCILTAY   | 293                       |
| Db   | 61   | LFVFGIEFVGVPVVTMTLCYARISRELFAKVPGGTQEQIRKRLCRKRTVLVLMCILTAY   | 120                       |
| Qy   | 294  | VLCWAPFYGFTIVRDFPTVFKVSKHYLTAFYIVVECIAMNSMINTLCFTVTKNDTVYK    | 353                       |
| Db   | 121  | VLCWAPFYGFTIVRDFPTVFKVSKHYLTAFYIVVECIAMNSMINTLCFTVTKNDTVYK    | 180                       |
| Qy   | 354  | KKIMLLHWKASYNGKSSADLDLKTIGHPATEEVDICIRLK 393                  |                           |
| Db   | 181  | KKMLRLHWRPSHYGKSSADLDLKTSGVPATEEVDICIRLK 220                  |                           |

|                    |   |   |                           |
|--------------------|---|---|---------------------------|
| RESULT 12          |   |   |                           |
| Q9VB87             | ID  | Q9VB87                                  | PRELIMINARY; PRT: 449 AA. |
| AC                 | Q9VB87  |   |                           |
| DT                 | 01-MAY-2000   | (TRENBLrel. 13, Created)                |                           |
| DT                 | 01-OCT-2002   | (TRENBLrel. 22, Last sequence update)   |                           |
| DT                 | 01-MAR-2003   | (TRENBLrel. 23, Last annotation update) |                           |
| DE                 | CG5811 protein.   |   |                           |
| GN                 | NEPR OR CG5811.   |   |                           |
| OS                 | Drosophila melanogaster (Fruit fly).                                    |   |                           |
| OC                 | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;           |   |                           |
| OC                 | Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;              |   |                           |
| OC                 | Ephydroidea; Drosophilidae; Drosophila.                                 |   |                           |
| OX                 | NCBI_TaxID=7227;  |   |                           |
| RN                 | [1]   |   |                           |
| RP                 | SEQUENCE FROM N.A.  |   |                           |
| RC                 | STRAIN=Berkeley;  |   |                           |
| RX                 | MEDLINE=20196006; PubMed=10731132;                                      |   |                           |
| RA                 | Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,         |   |                           |
| RA                 | Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,         |   |                           |
| RA                 | Sutton G.G., Levits S.E., Richards S., Ashburner M., Henderson S.N.,    |   |                           |
| RA                 | Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,           |   |                           |
| RA                 | Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D., |   |                           |
| RA                 | Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,   |   |                           |
| RA                 | Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,   |   |                           |
| RA                 | Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,     |   |                           |
| RA                 | Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,        |   |                           |
| RA                 | Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,          |   |                           |
| RA                 | Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,   |   |                           |
| RA                 | Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,           |   |                           |
| RA                 | de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,       |   |                           |
| RA                 | Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  |   |                           |
| RA                 | Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  |   |                           |
| RA                 | Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,        |   |                           |
| RA                 | Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,            |   |                           |
| RA                 | Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,          |   |                           |
| RA                 | Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,           |   |                           |
| RA                 | Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  |   |                           |
| RA                 | Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,        |   |                           |
| RA                 | Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,        |   |                           |
| RA                 | Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,            |   |                           |
| RA                 | Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,         |   |                           |
| RA                 | Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,       |   |                           |
| RA                 | Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,         |   |                           |
| RA                 | Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,      |   |                           |
| RA                 | Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,        |   |                           |
| RA                 | Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,         |   |                           |
| RA                 | Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,              |   |                           |
| RA                 | Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,       |   |                           |
| RA                 | Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,               |   |                           |
| RA                 | Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,       |   |                           |
| RA                 | Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,    |   |                           |
| RA                 | Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  |   |                           |
| RA                 | Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;                        |   |                           |
| RT                 | "The genome sequence of Drosophila melanogaster.";                      |   |                           |
| RL                 | Science 287:2185-2195(2000).  |   |                           |
| [2]                |   |   |                           |
| SEQUENCE FROM N.A. |   |   |                           |
| RA                 | Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,          |   |                           |
| RA                 | Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,       |   |                           |
| RA                 | Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,       |   |                           |
| RA                 | Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,      |   |                           |
| RA                 | Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,      |   |                           |
| RA                 | Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,              |   |                           |
| RA                 | Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,           |   |                           |
| RA                 | Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,         |   |                           |
| RA                 | McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,     |   |                           |
| RA                 | Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,                  |   |                           |
| RA                 | Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,        |   |                           |
| RA                 | Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,              |   |                           |
| RA                 | Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;        |   |                           |
| RT                 | "Sequencing of Drosophila melanogaster genome.";                        |   |                           |



DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR InterPro: IPR006162; Ppantne\_attach.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODOPS.  
DR PROSITE: PS00237; G.PROTEIN.RECEP\_FL1; 1.  
DR PROSITE: PS0262; G.PROTEIN.RECEP\_FL2; 1.  
DR PROSITE: PS00112; PHOSPHOPANTHETHEINE; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 465 AA; 52294 MW; 13C03A4C2DC47F47 CRC64;

Query Match 19.5%; Score 401; DB 5; Length 465;  
Best Local Similarity 26.3%; Pred. No. 4.8e-29;  
Matches 100; Conservative 79; Mismatches 145; Indels 56; Gaps 10;

Qy 11 NATWTSF-----LSVLNPHGA-----HATSF----- 33  
Db 5 NSENSTSLFGIKRHADYTGPHSAHDVIDPSNTSVYVDHASNYESVLSTSTLMLKLTDL 64  
Qy 34 --PNEFSYDMDLDEDEVDNSTRTEFA-----AKIVIGMALVGLMVCIGIGNFIFIAA 86  
Db 65 VTFNASEPD---PESNGSDTGGHAISQPMYARVIVLAVLILVAVGNNLFSYV 121  
Qy 87 LVRYKKLRLNLTNLIAIAISDFLVAIVCCPFEMDYVYVYVQLSWNEHGHVLCSTVNTLRV 146  
Db 122 IVMPFKRSVTNLFLLNLAISDIKAVICNPFAPFANLI--LLXWPGYGEFQCVVYIYQV 180  
Qy 147 SLXYSTNALLAIAIDRYLAIVHPLPRMKCOTATGLIALVWTVSILIAIPSAVFTTETVL 206  
Db 181 AVFLSATLVAMSDVRVAILKPRPLSKRAFAITWATWILSLNPLETAI----TSR 236  
Qy 207 VIVKQEKIFCGQIPWDOOLYKYKSYFLFIFGIEFVGVVVTMTLCYARISRELWFKAVPG 266  
Db 237 VTQSGNSTGLCLEHFENHDHNYI--YSIVIMMLQYFVPLAVITWNTHIGYIWMKKTGP 294  
Qy 267 FQTEQIKRLRC--RRKTVLVMCLITLAVLCWAPFYGFTIVROFFPVFKKHYLTAFY 325  
Db 295 EAEDRRMRAASRRRLKMLIIIVYAVCWLPVHVITLVGDHNPDIY-NQPHANVVL 353  
Qy 326 IVECIANSNMTLCFVTV 345  
Db 354 CAOWLAMSHSCYNPFVYFSL 373

## RESULT 15

Q94736 ID Q94736 PRELIMINARY; PRT; 678 AA.  
AC Q94736;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Tachykinin-like receptor.  
OS Stomoxys calcitrans (Stable fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;  
OC Muscidae; Stomoxys.  
OX NCBI\_TaxID=35570;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97269265; PubMed=9114446;  
RA Guerrero F.D.;  
RT "Transcriptional expression of a putative tachykinin-like peptide  
RT receptor gene from stable fly.";  
RL Peptides 18.1-5(1997).  
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; U52347; AAB07000.1; -  
DR HSSP; P02699; 1F88.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODOPS.  
DR PROSITE; PS00237; G.PROTEIN.RECEP\_FL1; 1.  
DR PROSITE; PS0262; G.PROTEIN.RECEP\_FL2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.

SQ SEQUENCE 678 AA; 75279 MW; FC3EIF4C8050400A CRC64;

Query Match 19.4%; Score 399.5; DB 5; Length 678;  
Best Local Similarity 28.6%; Pred. No. 1e-28;  
Matches 110; Conservative 76; Mismatches 150; Indels 49; Gaps 14;

Qy 7 PMDDNATNTSTSLSVLNPBGHAHATSPFENFS-----YSDDMPLDEDEDVNSR-- 56  
Db 98 FMYDMCNOSSL-----SSPSSA--AASFAPSSSDSDSGASSYNCSSLLGSSNAFNASN 152  
Qy 57 -TFFAAKI-----VIGMALVGLMVCIGI--GNFIFIAALVRYKKLRLNLTNLIAIAIS 107  
Db 153 DTFIDISFILPWRQVLWSILYGVVIVATGGNLJVMVIVITTKRMRTVNTYFIVNLSIA 212  
Qy 108 DELVAIVCCPFEMDYVYVYVQLSWNEHGHVLCSTVNYLRTVSLYVSTNALLAIAIDRYLAIV 167  
Db 213 DAMYSSLNVTF--SYIYMLDNNAWAFGQLYCKISQFIATLSISASVFTLMAISIDRYVAIN 270  
Qy 168 HPLRPRMKCOTATGLIALVWTVSILIAIPS--AYPTTETVLVIVKQEKIFCGQIWP---- 222  
Db 271 KPLRPRMKSRNLGIAAVIWIASAIISCPMLLFYTEE--VASKGIRTVCFLEWPDGSM 328  
Qy 223 --VDOOLYKYKSYFLFIFGIEFVGVVVTMTLCYARISRELWFKAVPGFQTEQIKRLRCRR 280  
Db 329 NHSNQETVYNTILFMI---LTYLEVVISMTATYSRVGLELWGSKAIGETTPROVENYKSKR 385  
Qy 281 KTVLVMCLITLAVLCWAPFYGFTIVRDEFP---TVFVKEKHVLTAFYIVECIANSNM 336  
Db 386 RVVYKMMVVLIFVVCWLPFHAYFIVTSCYPAITETTFIOE-----VYLFYIWLANSNM 440  
Qy 337 INTLCFTVTKNDTVKYFKKIMLLHW 361  
Db 441 YNPITYCWMSRFRFGPK--NFFRW 463

Search completed: October 7, 2003, 09:53:01

Job time : 43 secs